Prosity: May 19, 1999

5.1.6 Compugen Ltd. GenCore version Copyright (c) 1993 - 2005

- protein search, using sw model OM protein Run on:

April 28, 2005, 13:57:35 ; Search time 122.5 Seconds (without alignments) 56.830 Million cell updates/sec

US-10-009-317A-32

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_16Dec04: geneseqp1980s:* geneseqp1990s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

| | | | | | SUMMAKIES | |
|---------------|-------|----------------|--------|-----|--------------|---------------------|
| Result No. | Score | Query Match | Length | DB | ID | Description |
| | 116 | 100 | | . 4 | AAR35046 | Ashasan46 Thera def |
| 10 | 911 | | 9 - | • и | ABDE 3 2 0 E | A Antion |
| 9 ~ | 116 | 100 | 9 60 | ια | AD035230 | |
| 9 4 | 111 | 95.7 | 18 | ο α | . ADO35240 | Rhesus |
| · ru | 103 | 88.8 | 18 | 'n | ABP53299 | 0 |
| 9 | 101 | 87.1 | 18 | 4 | AAB35030 | |
| 7 | 101 | 87.1 | 18 | Ŋ | ABP53297 | |
| 8 | 101 | 87.1 | 18 | 9 | AAE33866 | |
| 6 | 101 | 87.1 | 18 | 7 | ADD95202 | Add95202 Cyclic de |
| 10 | 101 | 87.1 | 18 | ω | ADD35357 | 7 |
| 11 | 101 | 87.1 | 18 | œ | ADG70012 | 2 Rhesus |
| 12 | 101 | 87.1 | 18 | æ | AD035229 | 9 Rhesus |
| 13 | 101 | 87.1 | 18 | ω | AD035238 | Ado35238 Rhesus th |
| 14 | 101 | 87.1 | 18 | œ | AD035239 | Ado35239 Rhesus th |
| 15 | 101 | 87.1 | 18 | æ | AD035250 | Ado35250 Rhesus th |
| 16 | 101 | 87.1 | 38 | ω | AD035263 | Ado35263 Monkey RT |
| 17 | 100 | 86.2 | 18 | œ | AD035255 | Ado35255 Rhesus th |
| 18 | 93 | 80.2 | 18 | 9 | AAE33805 | Aae33805 I2Y retro |
| 19 | 93 | 80.2 | 7 | 9 | AAE33806 | Aae33806 I11Y retr |
| 20 | 93 | 80.2 | - | œ | ADN08180 | Adn08180 Human ret |
| 21 | 93 | 80.2 | 1 | æ | ADN08181 | Adn08181 Human ret |
| 22 | 91 | 78.4 | 18 | 4 | AAB35037 | Aab35037 Rhesus ma |
| 23 | 90 | 77.6 | 18 | 'n | ABP53294 | Abp53294 Synthetic |
| 24 | 90 | 77.6 | 18 | 9 | AAE33801 | |
| 25. | 90 | 77.6 | 18 | 9 | AAE33863 | Aae33863 Enantio-r |

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Gaps

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Query Match
100.0%; Score 116; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 8.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels

Sequence 18 AA;

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| Adno8176 Human ret Ado5229 Rhesus th Abp53298 Anti-vira Aau31804 Enantio-R Aae33802 RNK retro Adno8177 Human ret Aab55047 Theta def Abp53296 Anti-vira Ado35242 Rhesus th Ado35242 Rhesus th Ado35242 Rhesus th Ado35242 Rhesus th Ado35246 Rhesus th Aae33804 115X retro Ado35256 Rhesus th | |
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| ADNO 8176 ADO3 5249 ABE 53298 AAR93 3864 AAR3 3864 AAR3 3802 AAR3 5047 AAR3 5047 AAR3 5242 ADO3 5241 AAR3 3803 AAR3 3803 AAR3 3803 AAR3 3803 AAR3 3807 AAR3 3807 AAR3 3807 | |
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ALIGNMENTS

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The present invention provides theta defensin peptides and analogues which have antimicrobial activity. They can be used in the treatment of bacterial, viral, fungal, protozoan and helminthic infections, in dislifectants and as food preservatives
                                                                                                                                                                                                                                                                                    Theta defensin; antimicrobial; cyclic; bacterium; fungus; protozoan; virus; helminth; disinfectant; food preservative; analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel theta defensin peptide with antimicrobial activity against
bacteria, yeast, fungi, protozoa and viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouellette AJ;
                                                         AAB35046 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 15; Fig 16; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Selsted ME, Tang Y, Yuan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-00309487.
                                                                                                                                                                                                                                    Theta defensin SEQ ID NO: 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAY-2000; 2000WO-US012842.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200068265-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                           27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-NOV-2000.
                                                                                                                  AAB35046;
RESULT 1
AAB35046
ID AAB3
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GPCRCICTRGFCRCICTR 18

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The present invention describes a method (M1) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in amphipathic alphabelical structure in a lipid environment for reducing the infectivity of a virus. (I) can have viruled and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-viral resistance. (I) can be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral proliferation in a subject tharbouring a latent virus, controlling virus spread within a virally-infected subject (VS), reducing virus burden in a vS, reducing virus population regardless of viral infection status, or inducing latency in a vS, (b) reducing the infectivity of a virus; and (c) rendering virus contaminated tissue or fluid sample safe for use, or reducing the number of infectious virus particles in a population of viruses. (MI) is useful for reducing the infectivity of a virus in sheep, cattle, horses, swine, cats, fowl and humans e.g. an enveloped virus infecting humans such as human intervired peptide is human intervired peptide is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      administered to a patient who is immunosuppressed or to a subject who is not infected with the virus, where the first anti-viral peptide is administered prior to or subsequent to the virus contacting the subject the anti-viral peptide is most preferably administered to a subject who
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                is chronically, latently or acutely infected with the virus. The present sequence represents a rhesus monkey theta defensin anti-viral peptide, which is given in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                      Anti-viral; viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maury W, Stapleton J, Stinski M, Roller R, Mccray PB, Tack
                                                                                                                                                                                                                                                                                                                 Anti-viral theta defensin peptide RTD-2 SEQ ID NO:28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 10; 65pp; English
                                                                         ABP53295 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2001; 2001US-0265270P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-2002; 2002WO-US002435.
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                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Macaca mulatta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200260468-A2.
                                                                                                                                                                                                                                    13-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                                                                                                      ABP53295;
                            NAME OF THE PROPERTY OF THE PR
RESULT 2
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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD03523-AD03525. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as the peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have
                                                                                                                                                                                           antimicrobial; antiinflammatory; antibacterial; virucide; fundicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; fundection; haemolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents the rhesus monkey wild-type theta defensin RTD-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel theta defensin analog useful for reducing or inhibiting growth survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                   Monkey; Rhesus theta defensin; RTD-2; antimicrobial peptide; cyclic;

    .18
/note= "The peptide is cyclised by a covalent link
between these two residues"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; SEQ ID NO 2; 46pp; English.
                                                                                                                                                Rhesus theta defensin peptide, RTD-2.
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                               ADO35230 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-APR-2003; 2003US-00427715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-2002; 2002US-0377071P.
                                                                                                         15-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  3. .16
5. .14
7. .12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Selsted ME, Tran DQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-167945/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JS2004014669-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                      Macaca mulatta.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JAN-2004.
                                                                      ADO35230;
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RESULT 3
               AD035230
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Gaps

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100.0%; Score 116; DB 5; Length 18; 100.0%; Pred. No. 8.5e-06; ive 0; Mismatches 0; Indels

Length 18;

100.0%; Score 116; DB 8; 100.0%; Pred. No. 8.5e-06;

18; Conservative

Matches

Query Match Best Local Similarity

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                                                                                                                                                                     Monkey, Rhesus theta defensin, RTD; antimicrobial peptide, antimicrobial, antinflammatory; antibacterial, virucide, fungicide, food; contact lens solution; eye wash solution, inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel theta defensin analog useful for reducing or inhibiting growth survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
 ö
 0; Indels
                                                                                                                                                                                                             food preservative, bacterial infection, viral infection, fungal infection, haemolytic activity.
                                                                                                                                                  defensin analogue peptide aRTD-2-OH.
Mismatches
                                                                                                                                                                                                                                                                                                                              /note= "Hydroxylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 14; 46pp; English.
                                                                                                                                                                                                                                                                          Location/Qualifiers
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0
                                                                                        ADO35240 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                                                        30-APR-2003; 2003US-00427715
                                                                                                                                                                                                                                                                                                                                                                                                            30-APR-2002; 2002US-0377071P
                     GFCRCICTRGFCRCICTR
                                                                                                                               (first entry)
18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tran DQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-167945/16.
                                                                                                                                                                                                                                                                                    Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                US2004014669-A1
                                                                                                                                                                                                                                              Macaca mulatta
                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                   Rhesus theta
                                                                                                                                15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                    22-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Selsted ME,
                                                                                                                                                                                                                                                       Synthetic.
                                                                                                           AD035240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           object.
Matches
                                                                               AD035240
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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival

of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The spectices are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present

sequence represents a Rhesus theta defensin analogue peptide

Sequence 18 AA

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rime present. All comprising a theta-defensin peptide in an amphipathic alpha-
ce peptide (I) comprising a theta-defensin peptide in an amphipathic alpha-
ce helical structure in a lipid environment for reducing the infectivity of
ce a virus. (I) can have virucide and anti-HIV activities, and can be used
correction of a virus and so can be used for; (a) protecting or
creating subject from a viral infection, preventing recurrent virus
correction in a subject harbouring a latent virus, controlling virus
spread within a virally-infected subject (VS), reducing virus burden in a
correction in a subject than a VS, reducing precentage of VS in a
correction virus shed from a VS, reducing virus burden in a
correction virus shed from a VS, reducing virus burden in a
correction virus shed from a VS, reducing precentage of VS in a
corpulation regardless of viral infection status, or inducing latency in a
corpulation regardless of viral infection status, or inducing the number
corrections virus particles in a population of viruses. (MI) is useful
corrections virus particles in a population of viruses, swine,
cots, fowl and humans e.g. an enveloped virus infecting humans such as
cuts, fowl and humans e.g. an enveloped virus infecting humans such as
contaminatered to a patient who is immunosuppressed or to a subject who is
contaminatered prior to or subsequent to the virus or activity of a dministered prior to or subsequent to the virus contacting the subject.

The anti-viral peptide is most preferably administered to a subject who is contaminated represents a chimannal/rhesus monkey theta defensin anti-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention describes a method (M1) of using a first anti-viral
                                                                                                                                                                                                                                                                                                                                                                                                       Anti-viral; viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
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                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                   Anti-viral chimeric theta defensin peptide H/RTD-2 SEQ ID NO:32
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0
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  Score 111; DB 8; Length 18
Pred. No. 2.8e-05;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maury W, Stapleton J, Stinski M, Roller R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 10; 65pp; English.
                                                                                                                                                                                                                                       ABP53299 standard; peptide; 18 AA
                                            ;
0
                                                                                      18
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01-AUG-2001; 2001US-0309368P.
Query Match
Best Local Similarity 94.4%;
                                                                                    1 GFCRCICTRGFCRCICTR
                                                                                                                              1 GFCRCTCTRGFCRCICTR
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                                            17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca mulatta.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
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                                            Matches
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us-10-009-317a-32.rag

ABP53297 standard; peptide; 18 AA.

13-NOV-2002 (first entry)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                     Gaps
                                                                                                                                                                                     fungus; protozoan; analogue.
viral peptide, which is given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                         Novel theta defensin peptide with antimicrobial activity against
bacteria, yeast, fungi, protozoa and viruses.
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                                                                                                                                                                                                                                     /note= "peptide bond cyclises the molecule" 3..16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 18;
                                      Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                    2; Indels
                                                                                                                                                                                     Theta defensin; antimicrobial; cyclic; bacterium; virus; helminth; disinfectant; food preservative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87.1%; Score 101; DB 4; Lu
83.3%; Pred. No. 0.00032;
ive 1; Mismatches 2;
                                     Score 103; DB 5;
Pred. No. 0.0002;
); Mismatches 2
                                                                                                                                                                                                                                                                                                                                                           Ouellette AJ;
                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                        AAB35030 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 4; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GFCRCICTRGFCRCICTR 18
                                                                    1 GFCRCICTRGFCRCICTR 18
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                                                                                                                                                                                                                                                                                                             10-MAY-2000; 2000WO-US012842.
                                    88.8%;
88.9%;
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                                                                                  1 GICRCICTRGFCRCICGR
                                                                                                                                                                      Theta defensin SEQ ID NO: 1.
                                                                                                                                                      (first entry)
                                  Query Match
Best Local Similarity 88.9
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15; Conservative
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                                                                                                                                                                                                                                                                                                                                                            Tang Y,
                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-031853/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 AA;
                      Sequence 18 AA;
                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                               WO200068265-A1
                                                                                                                                                                                                                                                                                                                             10-MAY-1999;
                                                                                                                                                                                                            Unidentified
                                                                                                                                                       27-MAR-2001
                                                                                                                                                                                                                                                                                               16-NOV-2000.
                                                                                                                                                                                                                                  Cross-links
                                                                                                                                                                                                                                                                                                                                                            Selsted ME,
        invention
                                                                                                                                        AAB35030;
                                                                                                                                                                                    Theta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                         RESULT 6
                                                                                                                  AAB35030
SXSS
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RESULT 7 ABP53297

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The present invention describes a method (M1) of using a first anti-viral comprising a theta-defensin peptide in an amphipathic alphace belical structure in a lipid emvironment for reducing the infectivity of a virus. (I) can have virucide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-viral resistance. (I) can be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject tharbouring a latent virus, controlling virus is spread within a virally-infected subject (VS), reducing virus shed from a VS. reducing percentage of VS in a VS. reducing virus shed from a VS. reducing percentage of VS in a VS. reducing virus shed from a VS. reducing virus infection status, or inducing latency in a CS population regardless of viral infection status, or inducing latency in a CS infectious virus particles in a population of viruses. (M1) is useful of infectious virus particles in a population of viruses, whine, cate, fewl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is a daininistered to a patient who is immunosuppressed or to a subject who is containinistered to a patient who is immunosuppressed or to a subject who is immunosuppressed or to a subject who is immunosuppressed or can anti-viral peptide is most preferably administered to a patient who is immunosuppressed or to a subject who is immunosuppressed or can anti-viral peptide is most preferably administered to a patient who is immunosuppressed or can subject who is expensed or to a subject who is expensed o
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                                                                          Anti-viral; viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Pred. No. 0.00032;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mccray PB,
Anti-viral theta defensin peptide RTD-1 SEQ ID NO:30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maury W, Stapleton J, Stinski M, Roller R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 10; 65pp; English
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01-AUG-2001; 2001US-0309368P.
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Best Local Similarity 83.3
Matches 15; Conservative
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                                                                                                                                                                                                                                                                     Macaca mulatta.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                             WOZ00260468-A2.
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Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
The invention relates to novel retrocyclin peptides. Peptides and methods of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel antibiotics. The invention is also useful in gene therapy. The present sequence is rhesus monkey theta defensin, RIDI peptide. This sequence is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacterial infection; human pathogen; holin; defensin;
peptide nucleic acid; PNA; penicillin; tetracycline; ampicillin;
kanamycin; antibiotic; antibacterial; antibiotic-resistance gene; cyclic.
                                                                                                                                                      Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; rhesus monkey; theta defensin 1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated retrocyclin peptide, useful for preventing retroviral infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually transmitted diseases, vaginosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87.1%; Score 101; DB 6; Length 18
83.3%; Pred. No. 0.00032;
                                                                                                                                                                                                                                                                                                                                                                                                                                Lehrer RI, Waring AJ, Cole AM, Hong TB;
                          AAE33866 standard; peptide; 18 AA.
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                                                                                                                                                                                                                                                                                                                                                                  18-APR-2001; 2001US-0284855P.
                                                                                                                          Macaca mulatta RTD1 peptide
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Query Match
Best Local Similarity 83.33,
Conservative
                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-103387/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18 AA;
                                                                                                                                                                                                                                     Macaca mulatta
                                                                                                                                                                                                                                                                  WO200285401-A1
                                                                                          16-APR-2003
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                                                           AAE33866;
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                                                                                                                                                                                                        RTD1.
             AAE33866
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This invention describes a novel conjugate for treating prokaryotic infections which comprises a transport mediator for passage through the prokaryotic cell membrane and a compound, directed against a prokaryote and intended for introduction into it. The prokaryote is a bacterium, especially one pathogenic in humans. The transport mediator is preferably fragment or variant or a defensin. The introduced compound is a peptide rucleic acid (PNA) that inhibits a gene, especially one implicated in resistance to penicillin, tetracycline, ampicillin or kanamycin. The conjugate has the structure transport mediator-spacer-PNA where the conjugate has the structure transport mediator-spacer-PNA where the spacer is poly (glycine and/or lysine), preferably containing 2-6 amino acids and the spacer is linked to the transport mediator through a cleavable disulfide bridge. The conjugates are administered together with an antibiotic, by parenteral, transdermal or subcutaneous routes. The products of the invention have antibacterial activity and are used, aspecifically in combination with antibiotics, for treating prokaryotic, specifically bacterial, infections, especially in combination with antibiotics and the pathogen is resistant to at least one antibiotic and then the PNA is directed against the antibiotic resistance gene. Where the PNA is directed against an estimative to co-administered antibiotics estimate and sensitive to co-administered antibiotics in e. 'old' antibiotics can be sequence represents a cyclic defensin fragment described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New conjugate of transport mediator and active agent, useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prokaryotic infections, especially by neutralizing antibiotic resistance

    .18
/note= "Residue 1 and residue 18 bond to form a cyclic

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waldeck W;
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
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Matches 15; Conservative
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    Key
Misc-difference
                                                                                                                                                            Disulfide-bond
Disulfide-bond
Disulfide-bond
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Gerdes

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for preparing a composition for treatment and/or prevention of bacteraemia for binding bacterial products such as lipopolysaccharide (LES) and/or lipteichonic acid (LTA), or for treatment and/or prevention of septic shock. RTD-1, isolated from immune cells of rhesus monkeys, has antibacterial, fungicide, virucide, immunomodulator and anticoagulant activity. RTD-1 inhibits microbial cell-wall biosynthesis and also binds to LPS and LTA. RTD-1 is useful for treatment and prevention of severe infections caused by Gram-positive or -negative bacteria and yeasts, or by viruses. RTD-1 combines four advantageous properties: a direct antimicrobial action, neutralisation of bacterial products (by binding), immunomodulation (reducing release of proinflammatory cytokines but increasing release of regulatory factors) and anticoagulant action, so
                                                                                                                                                                                                                                                                  Use of rhesus theta defensin-1 for treating or preventing bacteremia and septic shock, also for binding bacterial products and as immunomodulator and anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes the novel use of rhesus theta defensin-1 (RTD-1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .18 /note= "The peptide is cyclised by a covalent link between these two residues"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.1%; Score 101; DB 8; Length 18;
83.3%; Pred. No. 0.00032;
cive 1; Mismatches 2; Indels
                                                                                                                                                                              Brunner N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               provides a better and simpler treatment.
                                                                                                                                                                              Newton B, Labischinski H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhesus theta defensin peptide, RTD-1.
                                                                                                                                                                                                                                                                                                                                                          Example 1; SEQ ID NO 1; 28pp; German.
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                                            30-MAY-2003; 2003WO-EP005694.
                                                                                      13-JUN-2002; 2002DE-01026216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GFCRCLCRRGVCRCICTR
                                                                                                                               (FARB ) BAYER HEALTHCARE AG
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Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3. .16
5. .14
7. .12
                                                                                                                                                                                                                        WPI; 2004-071500/07.
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Disulfide-bond
Disulfide-bond
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Modified-site
24-DEC-2003
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                                                                                                                                                                              Ladel C,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel ophthalmic solution comprising a prostaglandin of the F-series and an antimicrobial peptide. A solution of the invention has hypotensive and ophthalmological activity. The solution is useful for the treatment of increased intraocular pressure, such as caused by glaucoma and for the reduction of ocular hypertension. The prostaglandin and the antimicrobial peptide work sprengistically, to provide beneficial reduction in the incidence of irritant and toxic side effects such as hyperaemia, irritation and inflammation of conjunctiva, ocular cell dysplasia, irridial melanocyte hyperplasia, and hyperplamentation, associated with the prior art prostaglandin compositions. The present sequence represents an antimicrobial peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rhesus theta defensin-1; RTD-1; bacteraemia; lipopolysaccharide; LPS;
lipteichonic acid; LTA; septic shock; antibacterial; fungicide; virucide;
immunomodulator; anticoagulant activity;
                                                              antimicrobial; ophthalmic; prostaglandin; hypotensive; ophthalmological; intraocular pressure; glaucoma; ocular hypertension; hyperaemia; irritation; inflammation; conjunctiva; ocular cell dysplasia; iridial melanocyte hyperplasia; hyperpigmentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ophthalmic solution useful for the treatment of increased intraocular pressure comprises a prostaglandin of the F-series and an antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 101; DB 8; Length Le. Pred. No. 0.00032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhesus theta-defensin-1 (RTD-1) peptide.
                    Antimicrobial peptide theta-defensin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 11; 11pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADG70012 standard; peptide; 18
                                                                                                                                                                                                                                                                                                                                                          21-MAR-2002; 2002US-0367071P.
                                                                                                                                                                                                                                                                                                                21-MAR-2003; 2003WO-US008935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                        (CAYM-) CAYMAN CHEM CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Johnson J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-011506/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
es 15; Conserv
                                                                                                                                                                                                                          WO2003079997-A2.
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                                                                                                                                                                              Unidentified
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                                                                                                                                                                                                                                                                      02-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maxey KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADG70012;
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Best Loc Matches

à g RESULT 11

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Monkey, Rhesus theta defensin, RTD; antimicrobial peptide; antimicrobial; antinflammatory; antibacterial; virucide; fungicide; food; contact lens solution, eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; thempore function; haemolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rhesus theta defensin analogue peptide aRTD-1-NH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADO35239 standard; peptide; 18 AA
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Matches 15; Conservative
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Disulfide-bond
Disulfide-bond
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Synthetic.
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ADO35239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defealled in the claims or appearing as ADO35239-ADO35257. The theta defealled in the claims or appearing are visibiliting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents the rhesus monkey wild-type theta defensin RTD-1.
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                                                                                                                                                                                                                                                                                          Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
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Pred. No. 0.00032;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhesus theta defensin analogue peptide aRTD-1-OH.
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                                                30-APR-2003; 2003US-00427715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.1%;
                                                                                              30-APR-2002; 2002US-0377071P
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Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                           (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                               WPI; 2004-167945/16.
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Disulfide-bond
Disulfide-bond
Modified-site
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  22-JAN-2004.
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                                                                                                                                                                                              Selsted ME,
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18 18

1 GFCRCLCRRGVCRCICTR 1 GFCRCICTRGFCRCICTR

Location/Qualifiers

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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as AD03529-AD035257. The theta detailed in the claims or appearing as AD03529-AD035257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of a microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or sood product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbistatic inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
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83.3%; Pred. No. 0.00032;
ive 1; Mismatches 2; Indels
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                                                                                                                                                                                       30-APR-2003; 2003US-00427715.
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                                                                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Selsted ME, Tran DQ;
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US2004014669-A1.
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                                                                                           22-JAN-2004
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Location/Qualifiers

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Key
Modified-site
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                                                                                                                                                                                                                                                                                                                             object.
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                                                                                                                                                                                                                                                                                                                     The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
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                                                                                                                                                                                                                                   Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhesus theta defensin analogue peptide RTD-1-26.
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                            /note= "Amidated"
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                                                                                                                               30-APR-2002; 2002US-0377071P.
                                                                                                      30-APR-2003; 2003US-00427715
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                                                                                                                                                         (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                 Tran DQ;
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                                                    US2004014669-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18 AA;
Disulfide-bond
Modified-site
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Synthetic.
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                                                                             22-JAN-2004.
                                                                                                                                                                                  Selsted ME,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADO35250;
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                                                                                                                                                                                                                                                                          object.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
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    18
/note= "The peptide is cyclised by a covalent link
between these two residues"

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Pred. No. 0.00032;
); Mismatches 2; Indels
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Matches 16; Conservative
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(c) 1993 - 2005 Compugen Ltd
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Sequence 1, Application US/09967808

Patent No. 6514727

APPLICANT: Seleted, Michael E.

APPLICANT: Tang, Yi-Quan

APPLICANT: Tang, Yi-Quan

APPLICANT: Ouellette, Andre J.

TITLE OF INVENTION: Same

TITLE OF INVENTION: Same

FILE REPRENCE: P-UC 3095

CURRENT PILING DATE: 2001-09-26

FURNERTY PILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin Ver. 2.0

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US-09-604-864-9
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Pred. No. 1.4e-05;
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CRGANISM: Macaca mulatta
US-09-309-487-1
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                                    US-09-309-487-1
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APPLICANT: Selsted, Michael E.
APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REFERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
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Sequence 9, Application US/09967808

Patent No. 6514727

GENERAL INFORMATION:

APPLICANT: Selsted, Michael E.

APPLICANT: Tang, Yi-Quan

APPLICANT: Vuan, Jun

APPLICANT: Vuan

APPLICANT: Vuan

TITLE OF INVENTION: Same

FILE REFERENCE: P-UC 3095

CURRENT APPLICATION NUMBER: US/09/309,487

PRIOR FILING DATE: 1999-05-10

PRIOR FILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 9

SEQ ID NO 9
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Best Local Similarity 77.8%; Pred. No. 0.00011;
Matches 14; Conservative 1; Mismatches 3;
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Best Local Similarity 81.2%; Pred. No. 0.00018;
Matches 13; Conservative 1; Mismatches 2;
                          ; OTHER INFORMATION: synthetic variant US-10-141-645-6
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ORGANISM: Artificial Sequence
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US-09-967-808-9
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US-09-309-487-9
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                                                                  Query Match 87.1%; Score 101; DB 4; Length 18; Best Local Similarity 83.3%; Pred. No. 1.4e-05; Matches 15; Conservative 1; Mismatches 2; Indels
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WS-10-141-645-5
; Sequence 5, Application US/10141645
; Patent No. 6713078
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ORGANISM: Artificial Sequence
                ; ORGANISM: Macaca mulatta
US-09-967-808-1
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                                                        y Sequence 2. Application US/10141645
y Patent No. 6713078
y Facent No. 6713078
y Facent No. 6713078
y Fabricant Robert Lehrer
y APPLICANT: Alan Waring
APPLICANT: Alexander Cole
y APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
y TITLE OF INVENTION: Antimicrobial Peptides
y TITLE OF INVENTION: Antimicrobial Peptides
y FILE REFERENCE: UCLA-001C1P
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT PILING DATE: 2002-05-06
y PRIOR APPLICATION NUMBER: US/18
y PRIOR APPLICATION NUMBER: Unassigned
y PRIOR FILING DATE: 2001-04-18
y RIOR FILING DATE: 2002-04-18
y RIOR APPLICATION NUMBER: Unassigned
y PRIOR FILING DATE: 2002-04-18
y NUMBER OF SEQ ID NOS: 125
y SOFTWARE: PastSEQ for Windows Version 4.0
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APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: 2002-05-06
FILE REFERENCE: 2002-05-06
PRIOR APPLICATION NUMBER: 00/284,855
PRIOR APPLICATION NUMBER: 00/284,855
PRIOR APPLICATION NUMBER: 000-04-18
PRIOR APPLICATION NUMBER: Uses OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
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72.2%; Pred. No. 0.00085;
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; OTHER INFORMATION: synthetic variant
US-10-141-645-2
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; OTHER INFORMATION: synthetic variant
US-10-141-645-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/10141645 Patent No. 6713078
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 75.0
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 73.3
Best Local Similarity 72.2
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                   JS-10-141-645-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                         GENERAL NO. 97.2070

APPLICANT: Robert Lehrer

APPLICANT: Alan Waring

APPLICANT: Alan waring

APPLICANT: Alexander Cole

APPLICANT: Teresa Hong

TITLE OF INVENTION: Retrocyclins - Antiviral and

TITLE OF INVENTION: Antimicrobial Peptides

FILE REPERENCE: UCLA-001CIP

CURRENT APPLICATION NUMBER: US/10/141,645

CURRENT APPLICATION NUMBER: 60/284,855

PRIOR PILING DATE: 2002-05-06

PRIOR FILING DATE: 2002-04-18

FRIOR FILING DATE: 2002-04-18

NUMBER OF SEQ ID NOS: 125

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 90; DB 4;
Pred. No. 0.00023;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Murphy, Christopher J.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: McAnulty, Jonathan F.
APPLICANT: Mead, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06468
CURRENT APPLICATION NUMBER: US/09/917,340
CURRENT APPLICATION NUMBER: 60/221,632
PRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2000-11-17
PRIOR FILING DATE: 2001-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-917-340-53
; Sequence 53, Application US/09917340
Patent No. 6696238
; GENERAL INFORMATION:
                                                                                                                                    Sequence 1, Application US/10141645
Patent No. 6713078
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3 GFCRCLCRRGVCRCIC 18
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 53
LENGTH: 18
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Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 77.6
Best Local Similarity 77.8
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-917-340-53
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Gaps

1 GICYCICGRGICRCICGR 18

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Query Match

64.7%; Score 75; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.011;
Matches 12; Conservative 0; Mismatches 6; Indels
                                                                                                                                               APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Tareaa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: CO/284,855
PRIOR APPLICATION NUMBER: Us/10/18
PRIOR APPLICATION NUMBER: Unassigned
PRIOR FILING DATE: 2002-04-18
SPRIOR PILING DATE: 2002-04-18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Alexander Cole
APPLICANT: Alexander Cole
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT PPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2002-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 75; DB 4;
Pred. No. 0.011;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: synthetic variant
US-10-141-645-8
US-10-141-645-8; Sequence 8, Application US/10141645; Patent No. 6713078
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.7%;
Matches 12; Conservative
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US-10-141-645-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.3%; Score 85; DB 4; Length 18; 72.2%; Pred. No. 0.00085; Live 0; Mismatches 5; Indels
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Patent No. 6713078

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT PILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR APPLICATION NUMBER: Us/soft SECOND OF THING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 18
                                                                 GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Aresa Hong
ITTLE OF INVENTION: Retrocyclins - Antiviral and
ITTLE OF INVENTION: Antimicrobial Peptides
FILE REPERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT APPLICATION NUMBER: 60/284,855
PRIOR PILING DATE: 2002-05-06
PRIOR FILING DATE: 2002-04-18
FRIOR FILING DATE: 2002-04-18
FRIOR FILING DATE: 2002-04-18
SROTHARE: APPLICATION NUMBER: Unassigned
FRIOR FILING DATE: 2002-04-18
STOR FILING DATE: 2002-04-18
FRIOR FILING DATE: 2002-04-18
STOR FILING DATE: 2002-04-18
FRIOR 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: synthetic variant
   Sequence 4, Application US/10141645 Patent No. 6713078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GFCRCICTRGFCRCICTR 18
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Matches 13; Conservative
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US-10-141-645-7
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Gaps ö

Length 18; 6; Indels ö

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1 GFCRCICTRGFCRCICTR 18

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RESULT 15

US-03-109-487-21

US-03-109-487-21

Sequence 21, Application US/09309487

Sequence 21, Application US/09309487

Sequence 21, Application US/09309487

GENERAL INFORMATION:

APPLICANT: Seleced, Michael E.

APPLICANT: Tangy X1-Quan

APPLICANT: Tangy X1-Quan

APPLICANT: Tangy X1-Quan

APPLICANT: Vuellette, Andre J.

TITLE OF INVENTION Antimicrobial Theta Defensins and Methods of Using Same

TITLE OF INVENTION NUMBER: US/09/309,487

CURRENT FILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

CURRENT FILING DATE: 1999-05-10

NUMBER OF SEQ ID NOS: 31

SEQ ID NO 21

LENGTH: 92

TYPE: PRT

ORGANISM: Macaca mulatta

US-09-309-487-21

Query Match

Best Local Smilarity 84.6*; Pred. No. 0.067;

Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps

QY

4 RCICTRGFCRIC 16

Db 65 RCICTRGFCRILC 77

Search completed: April 28, 2005, 14:23:42
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April 28, 2005, 14:13:43 ; Search time 91 Seconds (without alignments) 65.889 Million cell updates/sec
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1: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpaa} \( 1\) \text{USO7} \\ PUBCOMB.ppp: *

2: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpaa} \\ PUSO \text{PuBCOMB.ppp}: *

2: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpaa} \( 1\) \text{Puso} \\ PuBCOMB.pep: *

4: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpaa} \( 1\) \text{USO} \\ PUBCOMB.pep: *

5: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpaa} \( 1\) \text{USO} \\ PUBCOMB.pep: *

6: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpaa} \( 1\) \text{USO} \\ PUBCOMB.pep: *

7: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpaa} \( 1\) \text{USOB} \\ PUBCOMB.pep: *

8: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpaa} \( 1\) \text{USOB} \\ PUBCOMB.pep: *

10: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpaa} \( 1\) \text{USOB} \\ PUBCOMB.pep: *

11: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpaa} \( 1\) \text{USOB} \\ PUBCOMB.pep: *

13: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpaa} \( 1\) \text{USOB} \\ PUBCOMB.pep: *

14: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpaa} \( 1\) \text{USOD} \\ PUBCOMB.pep: *

15: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpaa} \( 1\) \text{USOD} \\ PUBCOMB.pep: *

16: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpaa} \( 1\) \text{USOD} \\ PUBCOMB.pep: *

16: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \text{USOD} \\ PUBCOMB.pep: *

18: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \text{USOD} \\ PUBCOMB.pep: *

18: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \text{USOD} \\ PUBCOMB.pep: *

19: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \text{USOD} \\ PUBCOMB.pep: *

19: \( cgn2 \frac{6}\) \text{prodata} \( 1\) \text{pubpa} \( 1\) \\ Pubpa \( 1\) \\ Pubpa \( 1\) \\ \\ Pubpa \( 1\) \
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1426032 seqs, 333106140 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Searched:
                                                                                                                                                                                                                                                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | | | | SUMMARIES | | | |
|---------------|-------|----------------|-------------------------------|----|------------------|-------------|------|-------|
| Result No. | Score | Query Match | * Query Match Length DB | DB | ID | Description | | |
| - | 116 | 100.0 | 18 | 14 | US-10-060-102-28 | Sequence | 28. | App. |
| 7 | 116 | 100.0 | 18 | 15 | US-10-427-715-2 | Sequence 2 | 7. | Appli |
| 3 | 116 | 100.0 | 18 | 15 | US-10-427-715-14 | | | Appl |
| 4 | 116 | 100.0 | 18 | 15 | US-10-721-839-28 | | 28, | App] |
| 2 | 103 | 88.8 | 18 | 14 | US-10-060-102-32 | | 32, | App] |
| 9 | 103 | 88.8 | 18 | 15 | US-10-721-839-32 | | 32, | App] |
| 7 | 101 | 87.1 | 18 | 14 | US-10-060-102-30 | | 30, | App] |
| 8 | 101 | 87.1 | 18 | 14 | US-10-313-994-1 | | | App 1 |
| 6 | 101 | 87.1 | 18 | 15 | US-10-427-715-1 | Sequence 1 | 1, 1 | App1 |
| 10 | 101 | 87.1 | 18 | 15 | US-10-427-715-12 | | | App] |
| 11 | 101 | 87.1 | 18 | 15 | US-10-427-715-13 | ٠. | 13, | App] |
| 12 | 101 | 87.1 | 18 | 15 | US-10-427-715-24 | • • | 24, | App] |
| 13 | 101 | 87.1 | 18 | 15 | US-10-721-839-30 | Sequence 3 | 30, | Appl |
| | | | | | | | | |

| Sequence 29, Appl | Sequence 6, Appli | σ, | 27 | H | 27 | Sequence 23, Appl | 31 | 31, | 53, | 5 | Ŋ | 67 | 29, | 'n | Sequence 15, Appl | 16, | Sequence 29, Appl | 3, 4 | 4 | Sequence 30, Appl | 7, | 13 | 20, | 17, | 31, | θ, | ď | 28 | 37 | 38 |
|---|-------------------|---------------|---------------|-----------------------|------------|-------------------|------------------------|------|-----|--------|------------------------|----------|------------------------|------------|------------------------|------------|-------------------|------------|-----------------------|-------------------|-----------------------|----|------------|------------|-----|----|------------|------------|------------|------------------------|
| 18 15 US-10-427-715-29 18 14 US-10-141-645-5 | US-10-141-6 | 14 US-10-313- | 14 US-10-060- | 18 14 US-10-141-645-1 | 15 US-10 | 15 US-1 | 18 14 US-10-060-102-31 | 15 U | 6 | 14 US- | 18 17 US-10-844-837-53 | 17 US-10 | 18 14 US-10-060-102-29 | US-10 | 18 15 US-10-427-715-15 | 7 | 15 US-10-721- | | 18 14 US-10-141-645-4 | 15 | 18 14 US-10-141-645-7 | 15 | 15 US-10-4 | | - | 14 | 14 | - | - | 18 15 US-10-427-715-38 |
| 14 100 86.2 15 93 80.2 | 16 93 80.2 | 17 91 78.4 | 18 90 77.6 | 19 90 77.6 | 20 90 77.6 | <u>ر</u> - | 22 88 75.9 | 8 | 7 | 7 | 26 87 75.0 | 7 | 28 86 74.1 | 29 86 74.1 | 30 86 74.1 | 31 86 74.1 | 32 86 74.1 | 33 85 73.3 | 34 85 73.3 | r. | 36 83 71.6 | e. | 7 | 39 82 70.7 | | | 42 75 64.7 | 43 74 63.8 | 44 73 62.9 | 45 73 62.9 |

ALIGNMENTS

Sequence 28, Application US/10060102 Publication No. US20030022829A1 GENERAL INFORMATION:

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APPLICANT: MAUNY, MENDY
APPLICANT: MAUNY, MENDY
APPLICANT: STRABLETON, JACK
APPLICANT: STRABLETON
APPLICANT: MCRAY, PAUL B.
APPLICANT: MCRAY, PAUL B.
APPLICANT: MCRAY, PAUL B.
APPLICANT: MCRAY, PAUL B.
TITLE OF INVENTION: OATHELICIDINS
FILE OF INVENTION: OATHELICIDINS
TITLE OF INVENTION: OATHELICIDINS
TITLE OF INVENTION: OATHELICIDINS
TITLE OF INVENTION: OATHELICIDINS
TITLE OF INVENTION: DAY, 0320, 368
PRIOR PAPLICATION NUMBER: 60/265,270
PRIOR PALING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 201
PRIOR SEQ ID NOS: 32
SOFTWARE: PAT
ORGANISM: Artificial Sequence
SEQ ID NOS: 32
SOFTWARE: PAT
ORGANISM: Artificial Sequence
TYPE: PRT
ORGANISM: Artificial Sequence
TYPE
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1 GFCRCICTRGFCRCICTR 18

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TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALITITLE OF INVENTION: CATHELICIDINS
TITLE OF INVENTION: CATHELICIDINS
FILE OF INVENTION: CATHELICIDINS
FILE PEPERBUCE: 10WA:035US
CURRENT APPLICATION NUMBER: US/10/060,102
PRIOR FILING DATE: 2003-01-25
PRIOR APPLICATION NUMBER: US/10/060,102
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VET: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: Peptide US-10-721-839-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 116; DB 15; Length 18; Best Local Similarity 100.0%; Pred. No. 1e-06; Matches 18; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                         STAPLETON, JACK
ROLLER, RICHARD
STINSKI, MARK
MCCRAY, PAUL B.
TACK, BRIAN
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                                                                                                                                        Sequence 2, Application US/10427715
Publication No. US20040014669A1
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
TILE REFERENCE: 66778-302 (UC5754)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: US 60/377,071
PRIOR APPLICATION NUMBER: US 60/377,071
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 116; DB 15; Length 18; 100.0%; Pred. No. 1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REFERENCE: 66778-302 (UC574)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: US 60/377,071
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100.0%; Pred. No. 1e-06;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENCTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: synthetic construct US-10-427-715-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 14, Application US/10427715; Publication No. US20040014669A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GFCRCICTRGFCRCICTR 18
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1 GFCRCICTRGFCRCICTR 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Selsted, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100.
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 18; Conservat
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US-10-427-715-14
                                                                                                                         US-10-427-715-2
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LENGTH: 18
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Gaps

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Sequence 32, Application US/10060102

Sequence 32, Application US/10060102

Publication No. US20030022829A1

GENERAL INFORMATION:

APPLICANT: STAPLETON, JACK

APPLICANT: STAPLETON, JACK

APPLICANT: STAPLETON, JACK

APPLICANT: STINSKI, MARK

APPLICANT: STINSKI, MARK

APPLICANT: TRICK, BRIDAN

TITLE OF INVENTION: NOVELEN: ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MARMAL

TITLE OF INVENTION: NOWHER: US/10/060,102

TITLE OF INVENTION: NOWHER: US/10/060,102

CURRENT APPLICATION NUMBER: 60/309,368

FRIOR APPLICATION NUMBER: 60/309,368

PRIOR FILING DATE: 2001-08-01

PRIOR FILING DATE: 2001-08-01

PRIOR FILING DATE: 2001-08-01

SEQ ID NO 32

SEQ ID NO 32

LENGTH: 18

LENGTH: 18
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CHER INFORMATION: Description of Artificial Sequence: Synthetic
CHER INFORMATION: Peptide
15-10-060-102-32
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88.9%; Pred. No. 2.9e-05;
Live 0; Mismatches 2;
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Best Local Similarity 88.9
Matches 16; Conservative
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; Sequence 28, Application US/10721839; Publication No. US20040086535A1; GENERAL INFORMATION:

US-10-721-839-28

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SQUENCE 1. Application US/10313994

| Publication No. US20030162718A1
| GENERAL INFORMATION:
| APPLICANT: Seleted, Michael E. |
| APPLICANT: Tang, Yi-Quan |
| APPLICANT: Own WHER: US. 310/313,994 |
| CURRENT PILING DATE: 1999-05-10 |
| PRIOR PILING DATE: 1999-05-10 |
| NUMBER OF SEQ ID NOS: 31 |
| SOFTWARE: Patentin Ver. 2.0 |
| SEQ ID NO. |
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    OTHER INFORMATION: Description of Artificial Sequence: Synthetic
    OTHER INFORMATION: Peptide
US-10-060-102-30

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                                                                                                                                             Length 18
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APPLICANT: Selected, Michael E.
APPLICANT: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REFERENCE: 66778-302 (UCS754)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT FILING DATE: 2003-04-30
PRIOR PLILING DATE: 2002-04-30
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                                                                                                                                          Score 101; DB 14;
Pred. No. 4.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 101; DB 14;
Pred. No. 4.9e-05;
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83.3%; Pred. No. 4.9e-05;
tive 1; Mismatches 2;
                                                                                                                                                                                                             1; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                    1 GFCRCLCRRGVCRCICTR 18
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                                                                                                                                          Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
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Best Local Similarity 83.3
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Best Local Similarity 83.3
Matches 15; Conservative
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ORGANISM: Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Macaca mulatta
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                                                                                                                                                                             Sequence 32, Application US/10721839

Publication No. US20040086535A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: APPLICANT: AND STINKEY, MARK
APPLICANT: APPLICANT: ACCEAY, PAUL B.
APPLICANT: TACK, BRIAN
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALI
TITLE OF INVENTION: CATHELICIDINS
FILE REFERENCE: 100Ma.035US
CURRENT APPLICATION NUMBER: US/10/721,839
CURRENT PILING DATE: 2003-01-02

FRIOR FILING DATE: 2001-08-01

PRIOR FILING DATE: 2001-08-01

PRIOR FILING DATE: 2001-08-01

PRIOR FILING DATE: 2001-08-01

PRIOR PILING DATE: 2001-08-01
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Publication No. US20030022829A1

GENERAL INFORMATION:

APPLICANT: STAPLETON, JACK

APPLICANT: ROLLER, RICHARD

APPLICANT: TACK, BRIAN

TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF FRIMATE THETA DEFENSINS AND MAMMALI

TITLE OF INVENTION: CATHELICIDINS

FILE REFERENCE: 1004-03-02

CURRENT APPLICATION NUMBER: 05/2-02-22

PRIOR APPLICATION NUMBER: 60/309,368

PRIOR APPLICATION NUMBER: 60/309,368

PRIOR APPLICATION NUMBER: 60/309,368

PRIOR APPLICATION NUMBER: 60/305,270

PRIOR PILING DATE: 2001-08-01

PRIOR PILING DATE: 2001-08-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: Description of Artificial Sequence: Synthetic; OTHER INFORMATION: Peptide US-10-721-839-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Best Local Similarity 88.9%; Pred. No. 2.9e-05;
Matches 16; Conservative 0; Mismatches 2;
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SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                      US-10-721-839-32
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LENGTH: 18
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LENGTH: 18
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US-10-721-839-30

Sequence 30, Application US/10721839

Publication No. US20040086535A1

GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STARLETON, JACK
APPLICANT: STINSKI, MARK
APPLICANT: STINSKI, MARK
APPLICANT: TOLLER, RICHARD
APPLICANT: TACK, BRIAN
TITLE OF INVENTION: OAVULLANTIVRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MARWAL
TITLE OF INVENTION: OAVULLANTIONS
TITLE OF INVENTION: OAVULLANTIONS
TITLE OF INVENTION: OAVULLANTIONS
TITLE OF INVENTION: OAVULLANTIONS
TITLE OF INVENTION WINDER: US/10/721,839
CURRENT PILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/309,368
PRIOR PILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATECHIN VOI. 21.
SEQ ID NO 30
LENGTH: 18
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US-10-721-839-30
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                     Sequence 24, Application US/10427715

Publication No. US20040014669A1

GENERAL INFORMATION:

APPLICANT: Selsted, Michael E.

APPLICANT: Tran, Dat Q.

TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs

TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs

TITLE OF INVENTION: Thereof, and Methods of Use

FILE REFERENCE: 66778-302(UC554)

CURRENT FILING DATE: 2003-04-30

PRIOR FILING DATE: 2002-04-30

NUMBER OF SEQ ID NOS: 41

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 18
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Pred. No. 4.9e-05;
1; Mismatches 2;
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Pred. No. 4.9e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: synthetic construct US-10-427-715-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87.1%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
Matches 15; Conservative
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Best Local Similarity 88.9
Matches 16, Conservative
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US-10-721-839-30
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TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REPERENCE: 65778-302 (UG5754)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT PILING DATE: 2003-04-30
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FABEUSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 18
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87.1%; Score 101; DB 15; Length 18;
Best Local Similarity 83.3%; Pred. No. 4.9e-05;
Matches 15; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 87.1%; Score 101; DB 15; Length 18; Best Local Similarity 83.3%; Pred. No. 4.9e-05; Matches 15; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: synthetic construct
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LOCATION: 18
OTHERION: at the C terminus
US-10-427-715-13
                                                                                                Sequence 12, Application US/10427715
Publication No. US20040014669A1
GENERAL INFORMATION:
APPLICANT: Seleted, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFCRCLCRRGVCRCICTR 18
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1 GFCRCLCRRGVCRCICTR 18
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LENGTH: 18
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US-UL-14-10-427-115-29

US-10-427-115-29

Sequence 29, Application US/10427715

Publication No. US20040014669A1

SEQUENCE INFORMATION:

APPLICANT: Selsted, Michael E.

APPLICANT: Tran, Dat Q.

TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs

FILE REFERENCE: 66778-302 (US5754)

CURRENT APPLICATION NUMBER: US/10/427,715

CURRENT APPLICATION NUMBER: US 60/377,071

PRIOR FILING DATE: 2002-04-30

NUMBER OF SEQ ID NOS: 41

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 29

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 86.2%; Score 100; DB 15; Length 18; Best Local Similarity 93.8%; Pred. No. 6.4e-05; Matches 15; Conservative 0; Mismatches 1; Indels
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Sequence 5, Application US/10141645

Sequence 5, Application US/10141645

BENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645

CURRENT FILING DATE: 2001-05-06

PRIOR FILING DATE: 2001-06-18

PRIOR FILING DATE: 2001-06-18

PRIOR FILING DATE: 2001-06-18

NUMBER OF SEC ID NOS: 125

SEC ID NOS: 125

LENGTH: 18
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; OTHER INFORMATION: synthetic variant
US-10-141-645-5
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ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 77.8
Matches 14; Conservative
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April 28, 2005, 14:00:51 ; Search time 26 Seconds (without alignments) 66.612 Million cell updates/sec Run on:

US-10-009-317A-32 116 1 GFCRCICTRGFCRCICTR 18

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | de | | | SUMMARIES | |
|---------------|-------|----------------|--------|----|-----------|--------------------|
| Result No. | Score | Query Match | Length | 13 | ΙD | Description |
| П | 87 | 75.0 | 18 | 7 | C59089 | theta defensin-1 |
| 7 | 64 | 55.2 | 76 | ~ | A59089 . | theta defensin la |
| 3 | 54.5 | 47.0 | 248 | ~ | E71602 | -0 |
| 4 | 54 | 46.6 | 290 | 7 | G72858 | |
| ß | 53 | 45.7 | 164 | 0 | T24272 | hypothetical prote |
| 9 | 53 | 45.7 | 188 | 7 | T15651 | |
| 7 | 52.5 | 45.3 | 73 | ~ | JC1066 | മ |
| œ | 51 | 44.0 | 72 | Н | TIMB | trypsin inhibitor |
| o | 51 | 44.0 | 419 | ~ | S69207 | vascular endotheli |
| 10 | 50.5 | 43.5 | 83 | ~ | S07405 | proteinase inhibit |
| 11 | | ٠ | 94 | ~ | JC2225 | Bowman-Birk protei |
| 12 | 50.5 | 43.5 | 103 | Н | TISYC2 | proteinase inhibit |
| 13 | 20 | 43.1 | 624 | Н | S54581 | probable membrane |
| 14 | 49 | 42.2 | 152 | ~ | T18975 | hypothetical prote |
| 15 | 49 | 42.2 | 157 | N | A25964 | thyroglobulin - ra |
| 16 | 49 | 42.2 | 1700 | 7 | S08167 | Balbiani ring 3 pr |
| 17 | 48 | 41.4 | 72 | Н | TIZB1P | inhi |
| 18 | 48 | 41.4 | 78 | H | TIZBIA | |
| 19 | 48 | 41.4 | 79 | Н | TIFB2 | proteinase inhibit |
| 20 | 48 | 41.4 | 83 | N | 807941 | proteinase inhibit |
| . 21 | 48 | 41.4 | 102 | ٦ | TISYD2 | proteinase inhibit |
| 22 | 48 | 41.4 | 160 | ~ | T25185 | hypothetical prote |
| 23 | 48 | 41.4 | 306 | 7 | S32834 | methylviologen-red |
| 24 | 48 | 41.4 | 476 | 7 | JC5042 | G protein-coupled |
| 25 | 48 | 41.4 | 1353 | Н | JH0675 | restrictin precurs |
| 26 | 47.5 | 40.9 | 77 | ~ | I48725 | Q300 protein - mou |
| 27 | 47.5 | 40.9 | 550 | N | PQ0618 | hypothetical prote |
| 28 | 47 | 40.5 | 113 | ~ | S56648 | д |
| 29 | 47 | 40.5 | 317 | ~ | JC7597 | chondromodulin-I 1 |

| | hypothetical prote | | gp330 protein prec | hypothetical prote | related to mutanas | reelin precursor - | proteinase inhibit | hypothetical prote | hypothetical prote | hypothetical prote | latent transformin | unknown protein, 9 | gene serrate prote | EF1 protein - fowl |
|--------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| JC7603 | T15840 | T22945 | T42737 | T33983 | T49781 | S58870 | 809415 | T17298 | T09052 | C96719 | A57293 | G96711 | S16148 | A31685 |
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| 317 | 2946 | 3191 | 4660 | 141 | 883 | 3461 | 146 | 511 | 761 | 792 | 1251 | 1307 | 1408 | 222 |
| 40.5 | 40.5 | 40.5 | 40.5 | 40.1 | 40.1 | 40.1 | 39.7 | 39.7 | 39.7 | 39.7 | 39.7 | 39.7 | 39.7 | 39.5 |
| 47 | 47 | 47 | 47 | 46.5 | 46.5 | 46.5 | 46 | 46 | 46 | 46 | 46 | 46 | 46 | 45.5 |
| 30 | 32 | 33 | 34 | 32 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

| RESULT 1 C59089 theta defensin-1 - rhesus macaque N;Alternate names: RTD-1 C;Species: Macaca mulatta (rhesus macaque) C;Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Acression: C59089 |
|---|
| R; Tang, Y.O.; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J. Science 286, 498-502, 1999 A;Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation A;Reference number: A59089; MUID:99453140; PMID:10521339 A;Accession: C59089 |
| A;Status: preliminary A;Molecule type: protein A;Molecule type: protein A;Molecule type: protein A;Molecule type: protein A;Note: this sequence is cyclically permuted by -6 residues from the sequence presented C;Comment: For the two contributing precursor sequences, see PIR:A59089 and PIR:B59089. C;Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing F;1-5/Region: theta defensin 1a-derived F;10-18/Region: theta defensin 1b-derived F;1-18/Cross-link: cyclopeptide (Arg-Cys) #status experimental F;2-11,4-9,13-18/Disulfide bonds: #status experimental F;9-10/Cross-link: cyclopeptide (Cys-Arg) #status experimental |
| Query Match 75.0%; Score 87; DB 2; Length 18; Best Local Similarity 86.7%; Pred. No. 0.00014; Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Qy 4 RCICTRGFCRCITR 18 Db 1 RCICTRGFCRCICRR 15 |

A59089

theta defensin la precursor - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Species: Macaca mulatta (rhesus macaque)
C;Species: Macaca mulatta (rhesus macaque)
C;Species: John 1999
R;Tang, Y.Q.; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J.
Science 286, 499-502, 1999
A;Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation A;Reference number: A59089; MUID:99453140; PMID:10521339
A;Accession: A59089
A;Accession: A59089
A;Accession: A59089
A;Accession: A59089
A;Accession: A59089
A;Conecule type: mRNA
A;Residues: 1-76 <ATAN>
A;Coss-references: UNIPROT:P82270; GB:AF191100; NID:g6137227; PIDN:AAF04389.1; PID:g61
C;Comment: For the complete mature sequence, see PIR:C59089.
C;Superfamily: mammalian defensin
C;Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing
F;1-20/Domain: signal sequence #status predicted <SIG>

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Thu Apr 28 17:53:32 2005

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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24272
R;Sims, M

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A,Residues: 1-188 <NHA>
A,Cross-references: UNIPROT:Q18238; EMBL:U58760; NID:g1330384; PID:g1330389; PIDN:AAB00
A,Experimental source: strain Bristol N2; clone C27A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    trypain inhibitor - mung bean
C;Species: Vigna radiata (mung bean)
C;Species: Vigna radiata (mung bean)
C;Date: 02-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 18-Aug-2000
C;Accession: JC1066
C;Accession: JC1066
C;Accession: JC1066
A;Title: Synthesis of mung bean trypsin inhibitor by the combination of the single straw A;Reference number: JC1066
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A; Residues: 1-73 cCHBA
A; Residues: 1-73 cCHBA
C; Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
C; Superfamily: Bowman-Birk proteinase inhibitor
C; Reywords: serine proteinase inhibitor
F;2-73/Product: trypsin inhibitor fatatus predicted <MAT>
F;14-40/Domain: Bowman-Birk inhibitor repeat homology <BBI>F;14-66/Domain: Bowman-Birk inhibitor repeat homology <BBI>F;14-66/Domain: Bowman-Birk inhibitor repeat homology <BBI>F;14-66/Domain: Bowman-Birk inhibitor repeat homology <BBIS>
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Pred. No. 6.9;
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Pred. No. 7.6;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45.7%;
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9; Conservative
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Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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A,Gene: CESP:C27A2.5
A,Map position: 2
A,Introns: 19/3; 91/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: CESP:T01B7.8
A;Map position: 2
A;Introns: 20/3; 90/2
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C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
A;Note: aBANA virus
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C;Accession: G72858
R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A;Accession: G72858
A;Accession: G72858
A;Accession: G72858
A;Accession: G72858
A;Accession: G72858
A;Accession: Preliminary
A;Molecule type: DNA
A;Residues: 1-290 cAXR>
A;Cross-references: UNIPROT:P41470; GB:L22858; NID:g510708; PIDN:AAA66700.1; PID:g559139
C;Genetics:
A;Gene: AcOrf-70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cypercises recasions. Fractional 13-Nov-1998 #text_change 09-Jul-2004
Cypercises 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
CyAccession: E71602
CyAccession: E71602
Foreign M. 1. Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; Ferthera, M.; Salaberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O. Science 282, 1126-1132, 1998
Arithe: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A; Reference number: A71600; MUD:99021743; PMID:9804551
A; Reference number: A71600; MUD:99021743; PMID:9804551
A; Residue: 17-248 cGAR>
A; Residue: 1-248 cGAR>
A; Residue: 1-248 cGAR>
A; Cross-references: UNIPROT:096282; GB:AE001428; GB:AE001362; NID:g3845316; PIDN:AAC7197
C; Genetics:
A; Gene: PFB0950w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable integral membrane protein PFB0950w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
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                       F;21-64/Domain: amino-terminal propeptide #status predicted <PRO>F;74-76/Domain: carboxyl-terminal propeptide #status predicted <CTP>
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                                                                                                                                  Length 76;
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                                                                                                                              Score 64; DB 2;
Pred. No. 0.2;
1; Mismatches 1
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                                                                                                                              Query Match
Best Local Similarity 83.3%;
Matches 10; Conservative
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Best Local Similarity
Matches 9; Conservat
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A;Molecule type: protein
A;Residues: 'X',104-120 <JOUZ>
R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.
submitted to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and Br
A;Reference number: S69208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: UNIPROT:P01063; EMBL:M20732; NID:g169944; PIDN:AAA33953.1; PID:g169-A;Note: the sequences of codons 8-13 and 14-27 are interchanged in the authors' transla R;Back, J.M.; Kim, S.I. S.I. shim, S.I. S.I. Submid to the EMBL Data Library, October 1992
A,Description: Nucleotide sequence of a cDNA encoding the soybean Bowman-Birk proteinas A,Reference number: $29559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Date: O.2-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S07405; S29608; S40113
R;Joudrier, P.E.; Foard, D.E.; Floener, L.A.; Larkins, B.A.
Bjant Mol. Bjol. 10, 35-42, 1987
A;Title: Isolation and sequence of cDNA encoding the soybean protease inhibitors PI IV
A;Reference number: S07405
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C;Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GDB:3890883; OMIM:601528
F;1-12/Domain: signal sequence #status predicted <SIG>
F;13-102/Domain: propeptide #status predicted <PRO>
F;103-419/Product: vascular endothelial growth factor C #status experimental <MAT>
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                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-419 <LEE>
A;Cross-references: EMBL:U43142; NID:g1150988; PIDN:AAA85214.1; PID:g1150989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:U58111; NID:g1373426; PIDN:AAB02909.1; PID:g1373427 C;Genetics:
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A,Molecule type: mRNA
A,Residues: 1-83 <BAE>
A,Cross-treferences: EMBL:X68705, NID:g18567; PIDN:CAA48656.1; PID:g18568
R,Giordano, A.; Delledonne, M.; Fogher, C.; Marchetti, S.
submitted to the EMBL Data Library, December 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: G02659
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-419 <MOR>
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submitted to the EMBL Data Library, May 1996
A,Reference number: H01557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 COCVCKRICPRNOPLNPGKCACECT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CRCICTR-----GFCRCICT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: serine proteinase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 36.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reference number: S40113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-83 <JOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-83 <GIO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Status: preliminary
                                                                                                                                                                                                                            A; Accession: S69208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: S07405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: $29608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: GDB: VEGFC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
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NyAlternate names: FLT4 ligand DHM
C;Specias: Home Sapiens (man)
C;Date: 27-Apr-1996 #sequence revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: S69207; S61795; $71443; S69208; G02659
R;Joukov, V.; Palusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, B.; Saksela, BMBO J. 151, 1751, 1996
A;Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand fc A;Reference number: S69207; MUD: 96201094; PMID: 8612600
A;Accession: S69207; MUD: 96201094; PMID: 8612600
A;Accession: S69207; MUD: 96201094; PMID: 8612600
A;Accession: S69207
A;Retus: nucleic acid sequence not shown
A;Noteule type: mRNA
A;Residues: 1-419 < JOUA
A;Cross-references: UMIPROT: P49767; EMBL:X84216; NID: 91177488; PIDN: CAA63907.1; PID: e221
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
A;Note: chig is a revision to the sequence from reference S61795
B;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela, BMBO J. 15, 290-298, 1996
A;Title: A novel vascular endothelial growth factor, VEGF-C, is a ligand for the Flt4 (VA)
A;Accession: S61795; MUD: 96178224; PMID: 8617204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             d.198-1, respectively
C;Comment: This inhibitor etoichiometrically inhibits trypsin in a molar ratio of 1:2.
C;Comment: This inhibitor retoichiometrically inhibitor; Bowman-Birk inhibitor repeat homology c;Superfamily: Bowman-Birk proteinase inhibitor
C;Keywords: duplication; serine proteinase inhibitor
F;13-19/Domain: Bowman-Birk inhibitor repeat homology cBB1>
F;10-65/Domain: Bowman-Birk inhibitor repeat homology cBB2>
F;12-66,13-28,16-62,18-26,36-43,40-55,45-31/Disulfide bonds: #status predicted
F;20/Inhibitory site: Lys (trypsin) #status predicted
F;47/Inhibitory site: Arg (trypsin) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Accession: A01301
A,Molecule type: protein
A,Rolecule type: protein
A,Rolecule type: protein
A,Cross-references: UNIPROT:P01062
A,Cross-references: UNIPROT:P01062
A,Note: three isoinhibitors are also found whose amino ends differ slightly from that a Lys-1, respectively
C,Comment: This inhibitor stoichiometrically inhibits trypsin in a molar ratio of 1:2.
C,Superfamily: Bowman-Birk proteinase inhibitor; Bowman-Birk inhibitor repeat homology
C,Keywords: duplication; serine proteinase inhibitor.
F,13-39/Domain: Bowman-Birk inhibitor repeat homology <BB1>
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                                                                                                                  ۳
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Vigna radiata (mung bean)
Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: A01301
R;Zhang, Y.; Luo, S.; Tan, F.; Qi, Z.; Xu, L.; Zhang, A.
Sci. Sin. 25, 268-277, 1982
A;Title: Complete amino acid sequence of mung bean trypsin inhibitor.
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                                         Length 73,
                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 72;
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A,Residues: 70-419 <JOUI>
A;Note: this sequence has been revised in reference S69207
A;Accession: S71443
                                         7
                                  Score 52.5; DB
Pred. No. 4.6;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match
Local Similarity 57.9%; Pred. No. 6
hes 11; Conservative 2; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                     trypsin inhibitor (Bowman-Birk) - mung bean
                                                                                                                                                                                  3 CR-CICTR---GFCRCI----CTR 18
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40 CKSCICTRSMPGKCRCLDT 58
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                                  45.3%;
                                  Query Match 45.3
Best Local Similarity 48.0
Matches 12, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A01301
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Matches
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A;Residues: 1-152 <WIL>
A;Cross-references: UNIPROT:Q9XVX3; EMBL:Z49886; PIDN:CAA90055.1; GSPDB:GN00020; CESP:C
A;Experimental source: clone C06A1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL: Z49702; NID: 9817859; PID: 91326013; GSPDB: GN000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 345-624 <LYE>
A;Cross-references: EMBL:Z49273; NID:g809577; PID:g809578; GSPDB:GN00013; MIPS:YMR119w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable membrane protein YMR119w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YM8564.01; hypothetical protein YM9718.18
C;Species: Saccharomyces cerevisiae
C;Date: 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S54581; S54488
R;Hunt, S.; Bowman, S.
submitted to the BMBL Data Library, May 1995
A;Reference number: S54510
A;Reference number: S54581
A;Reference Ltype: DMAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                          1;
F;42-68/Domain: Bowman-Birk inhibitor repeat homology <BBl>>
F;69-94/Domain: Bowman-Birk inhibitor repeat homology <BB2>
F;41-95,42-57,45-91,47-55,65-72,69-84,74-82/Disulfide bonds: #status predicted
F;49/Inhibitory site: Ala (elastase) #status predicted
F;76/Inhibitory site: Arg (trypsin) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C06Al.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18975
R;McMurray, A.
                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                 Length 103;
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                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Ke^words: transmembrane protein
F;83-98/Domain: transmembrane #status predicted <TM1>
F;120-136/Domain: transmembrane #status predicted <TM2>
F;211-227/Domain: transmembrane #status predicted <TM3>
F;237-253/Domain: transmembrane #status predicted <TM3>
F;278-294/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                 DB 1;
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A;Reference number: 219054
A;Accession: T18975
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                 ; Score 50.5; DE; Pred. No. 10; 1; Mismatches
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A;Map position: 13R
C;Superfamily: probable membrane protein YMR119w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A)Cross-references: UNIPROT:PS4074; EMBL:Z497A; Experimental source: strain AB972
R;Lye, G.; Churcher, C.M.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54014
A;Accession: S54488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              583 CRCFAICEDCRISLGLRGFSTCVCCR 608
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                                                                                                                                                                                                                                                                                                                                                                                                                                          17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 RCACTRSMPGQCRCLDT 87
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 58.8%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          4 RCICTR---GFCRCICT
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C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Date: 24.Apr-1984 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A22636; A01302
B;Hammond, R.W.; Foard, D.E.; Larkins, B.A.
J; Biol. Chem. 259, 9883-9890, 1984
J;Title: Molecular cloning and analysis of a gene coding for the Bowman-Birk protease in A;Reference number: A22489; MUID:84264652; PMID:608657
A;Contents: annotation
A;Reference number: A2489; MUID:84264652; PMID:6086657
A;Contents: annotation
A;Reference number: A2489; MUID:84264652; PMID:6086657
A;Contents: annotation
A;Reference number: A2489; MUID:84264652; PMID:6086657
A;Reference number: A2489; MUID:84264652; PMID:6086657
A;Reference number: A32540
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A;Contents: erratum
A;Contents: erratum
A;Contents: erratum
A;Accession: A22636
A;Molecule type: DNA
A;Residues: 1-103 <a href="https://docs.org/ldc.com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/pless/reserved-er-com/ple
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A/Molecule type: mRNA
C/Comment: This protein regulates endogeneous proteinase during germination, stores sulf
C/Comment: This protein regulates inhibitor; Bowman-Birk proteinase inhibitor
C/Comment: Sowman-Birk proteinase inhibitor
C/Comment: Signal sequence #status predicted <SIG>
F/19-94/Product: Bowman-Birk proteinase isoinhibitor CII #status predicted <MAT>
F/19-59/Domain: Bowman-Birk inhibitor repeat homology <BBI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: JC2225
K;Back, J.M.; Song, J.C.; Choi, Y.D.; Kim, S.I.
Biosci. Blotechnol. Biochem. 58, 843-846, 1994
A;Title: Nucleotide sequence homology of cDNAs encoding soybean Bowman-Birk type protein
A;Reference number: JC2224; MUID:94289861; PMID:7764974
                                                                                                 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bowman-Birk proteinase isoinhibitor C-II precursor (clone pB24) - soybean C;Species: Glycine max (soybean)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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             Length 83
                                                                                                 Indels
43.5%; Score 50.5; DB 2;
58.8%; Pred. No. 8.6;
iive 1; Mismatches 3;
                                                                                                                                                                                 4 RCICTR---GFCRCICT 17
                                                                                                                                                                                                                              4 RCICTR---GFCRCICT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RCACTRSMPGQCRCLDT 78
                                                Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 10; Conserv
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thyroglobulin - rat (fragments)
CiSpecies: Rattus norvegicus (Norway rat)
CiSpecies: Rattus norvegicus (Norway rat)
CiSpecies: OJUN-1989 #sequence_revision 30-JUN-1991 #text_change 11-Apr-1997
CiAccession: A25964
RiMusti, A.M.; Avvedimento, E.V.; Polistina, C.; Ursini, V.M.; Obici, S.; Nitsch, L.; CcArc. A111. A264 Sci. U.S.A. 83, 323-327, 1986
A; Title: The complete structure of the rat thyroglobulin gene.
A; Reference number: A25964; MUID:86094383; PMID:3455768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; MOLECULE TYPE: DNA
A; Residues: 1-157 <MUS.>
A; Residues: 1-157 <MUS.>
A; Residues: 1-157 <MUS.>
A; Residues: 1-157 <MUS.>
A; Note: the authors translated the codon GTG for residue 44 as Leu
C; Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homology
C; Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis
F; 35-60/Domain: thyroglobulin type I repeat homology (fragment) <THYI>
F; 134-138/Domain: thyroglobulin type I repeat homology (fragment) <THYI>
F; 25/Modified site: thyroxine (Tyr) #status predicted
                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Gaps
                                                                                                                                                                                                             ö
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42.2%; Score 49; DB 2; Length 157;
Best Local Similarity 32.0%; Pred. No. 20;
Matches 8; Conservative 4; Mismatches 5; Indels
                                                                                                                                  Query Match
42.2%; Score 49; DB 2; Length 152;
Best Local Similarity 50.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 GECWCVCSFFVPTCTSEGECYCVCS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GFCRCIC-----TRGFCRCICT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: April 28, 2005, 14:22:37 Job time : 28 secs
                                                                                                                                                                                                                                                                            1 GFCRCICTRGFCRCIC 16
                                                                                                                                                                                                                                                                                                                                            67 GGCGCCCKPRCCCCC 82
A;Gene: CESP:C06A1.6
A;Map position: 2
A;Introns: 22/3
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April 28, 2005, 13:58:25 ; Search time 114 Seconds (without alignments) 80.855 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                OM protein - protein search, using sw model
                                                                                                                                                                         Run on:
```

1612378 Total number of hits satisfying chosen parameters: 1612378 seqs, 512079187 residues 116 1 GPCRCICTRGFCRCICTR 18 Gapop 10.0 , Gapext 0.5 US-10-009-317A-32 **BLOSUM62** Perfect score: Scoring table: Sequence: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% .
Maximum Match 100%
Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description | P82270 macaca mula | mus | Q8ch20 mus musculu | Q9d9i2 mus musculu | Q9d4k2 mus musculu | Q949g1 oryza sativ | | Q9blj1 ciona intes | 096282 plasmodium | P41470 autographa | Q7seq2 neurospora | Q9nrb6 homo sapien | _ | Q95qy1 caenorhabdi | Q18238 caenorhabdi | Q17641 caenorhabdi | Q75nz5 chlamydomon | Q75n88 homo sapien | | | Q94uz6 leishmania | Q6ry99 rattus norv | | | | Q7prp5 anopheles g | Q9ui23 homo sapien | Q6ig37 drosophila | P01062 phaseolus a | Q6zgs2 homo sapien | _ |
|-------------------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------------------|-------------------|-------------------|-------------------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------|-------------------|--------------------|--------|--------|--------|--------------------|--------------------|-------------------|--------------------|--------------------|--------|
| SUMMALES | TD1A_MACMU | Q6P8T4 | Q8CH20 | Q9D912 | Q9D4K2 | Q949G1 | Q8VJ20 | Q9BLJ1 | 096282 | YO70 NPVAC | Q7SEQ2 | Q9NRB6 . | Q22048 | Q95QY1 | Q18238 | 017641 | Q75NZ5 | Q75N88 | Q75N87 | Q7PJ70 | Q94UZ6 | Q6RY99 | Q9PYQ3 | Q7QBV4 | Q8MZ55 | Q7PRP5 | Q9UI23 | Q61G37 | IBB_PHAAU | ŏez <u>ŏ</u> sz | 0912Н6 |
| DB | ٦ | ~ | ~ | ~ | ~ | 7 | ~ | ~ | ~ | ~1 | ~ | 0 | ~ | ~ | ~ | ~ | 7 | ~ | ~ | ~ | 0 | 7 | N | ~ | ~ | 7 | 7 | N | - | N | 7 |
| % Query Match Length DB | 16 | 168 | 168 | 168 | 173 | 274 | 163 | 937 | 307 | 290 | 991 | 174 | 164 | 166 | 188 | 197 | 602 | 1365 | 2871 | 129 | 273 | 512 | 99 | 146 | 161 | 1823 | 190 | 59 | 72 | 201 | 326 |
| % Query Match | 55.2 | 50.9 | 50.9 | 50.9 | 50.9 | 50.9 | 48.7 | 48.3 | 47.0 | 46.6 | 46.6 | 46.1 | 45.7 | 45.7 | 45.7 | 45.7 | 45.7 | 45.7 | 45.7 | 45.3 | 45.3 | 45.3 | 44.8 | 44.8 | 44.8 | 44.8 | 44.4 | 44.0 | 44.0 | 44.0 | 44.0 |
| Score | 64 | 29 | 59 | 59 | 59 | 59 | 56.5 | 10 | 54.5 | 54 | 54 | 53.5 | 53 | 23 | 53 | 53 | 53 | 53 | 53 | 52.5 | 52.5 | 52.5 | 25 | 52 | 52 | 52 | 51.5 | 51 | 51 | 51 | 51 |
| Result No. | п | 7 | ٣ | 4 | Ŋ | 9 | 7 | 80 | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | 18 | 19 | 20 | 21 | 22 | 23 | 24 | 25 | 56 | 27 | 28 | 29 | 30 | 31 |

| Q7pvn9 anopheles g | - | Q91ze3 rattus norv | | | P01063 glycine max | | Q8ru22 glycine soj | | Q6vz23 canarypox v | Q78xv0 brachydanio | Q781g4 neurospora | Q9ava3 pisum sativ | Q7ywv7 caenorhabdi |
|--------------------|------------|--------------------|-------------|--------|--------------------|-----------------|--------------------|--------|--------------------|--------------------|-------------------|--------------------|--------------------|
| Q7PVN9 | VEGC_MOUSE | Q912E3 | VEGC. HUMAN | Q6A1N6 | IBB2 SOYBN | Q8LC <u>9</u> 2 | QBRU22 | Q87BL8 | Q6V223 | Q7SXV0 | Q7S1G4 | Q9AVA3 | Q7YWV7 |
| 7 | ч | N | н | ~ | -4 | N | ~ | N | ~ | ~ | ~ | ~ | 7 |
| 336 | 415 | 415 | 419 | 482 | 83 | 91 | 109 | 168 | 222 | 379 | 1411 | 99 | 212 |
| 44.0 | 44.0 | 44.0 | 44.0 | 44.0 | 43.5 | 43.5 | 43.5 | 43.5 | 43.5 | 43.5 | 43.5 | 43.1 | 43.1 |
| 21 | 21 | 51 | 51 | 51 | 50.5 | 50.5 | 50.5 | 50.5 | 50.5 | 50.5 | 50.5 | 20 | 20 |
| 32 | 33 | 34 | 35 | 36 | 37 | 38 | 39 | 40 | 41 | 42 | 43 | 44 | 45 |

ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                           Tang Y.-Q., Yuan J., Oesapay G., Oesapay K., Tran D., Miller C.J., Ouellette A.J., Selsted M.B.,

"A cyclic antimicrobial peptide produced in primate leukocytes by the ligation of two truncated alpha-defensins.";
Science 286:498-502(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "CDNA cloning of three alpha-defensins and three demidefensins from rhesus monkey bone marrow.";

"CDNA cloning of three alpha-defensins and three demidefensins from rhesus monkey bone marrow.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: Active against the Gram-positive bacteria S.aureus and L.monocytogenes, Gram-negative bacteria S.typhimurium and E.coli ML35 and fungi C.albicans and C.neoformans in vitro.

-I- SUBUNIT: Forms a cyclic heterodimer composed of subunits A and B;

disulfide-linked.

-I- TISSUE SPECIFICITY: Expressed in bone marrow. Detected in promyelocytes, myelocytes and mature neutrophils and monocytes.

-I- DEVELOPMENTAL STAGE: Expression begins early during granulocyte
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., SEQUENCE OF 65-73, TISSUE SPECIFICITY,
DEVELOPMENTAL STAGE, AND DISULFIDE BONDS.
TISSUE=Bone marrow, and Leukocyte;
MEDLINE=99453140; PubMed=10521339; DOI=10.1126/science.286.5439.498;
                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
TDIA MACMU STANDARD; PRT; 76 AA.
P82270; Q9TU01;
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last amnotation update)
25-OCT-2004 (Rel. 45, Last annotation update)
Theta defensin-1, subunit A precursor (RTD-1a) (Demidefensin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           myelopoiesis.-!- PTM: This is a cyclic peptide.-!- SIMILARITY: Belongs to the corticostatin/defensin family.
                                                                                                                                                              Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF191100; AAF04389.1; -. EMBL; AF191102; AAF04391.1; -. EMBL; AF184157; AAF07924.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-Bone marrow;
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66 CRCCCYCRCCRCCSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         090912;
                                                                                        Q8CH20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9D912
                                                          RESULT 3
Q8CH20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Testis;

X Strusberg Factis;

X Strusberg R.L., Featigold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Featigold E.A., Grouse L.H., Derge J.G.,

X Alausner R.D., Collins F.S., Wagner L., Derge J.G.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Raha S.S., Loquellanno N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellanno N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Rosak S.A., McEwan P.J., McKernen K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                          Gaps
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                                                          Antibiotic, Defensin, Direct protein sequencing, Fungicide, Signal. SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                   Interchain (with C-66 of subunit B)
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                                                                                                                                                                                                           Score 64; DB 1; Length 76; Pred. No. 0.34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Indels
                                                                                                         Theta defensin-1, subunit A.
                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE.

JISSUES BROOK PROJECT;

Director MGC Project;

Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BC061079; AAH61079.1;

GPOITENCE 168 AA; 18947 MW; BOOFDJD27B9BF768 CRC64;
                                                                                                                                                                 T -> A (in Ref. 2).
BEA207932A030590 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                         G6P8T4;
05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
4931420D14Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.9%; Score 59; DB 2; 56.2%; Pred. No. 2.9; tive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              168 AA.
                                                                                                                                                                                                                                          1; Mismatches
               InterPro; IPR002366; Defensin propep. Pfam; PF00879; Defensin propep; 1. PROSITE; PS00269; DEFENSIN; FALSE NEG.
                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                 38
8242 MW;
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                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                       |||||||||||||||| :
RCICTRGFCRLL 76
                                                                                                                                                                                                                                                                       4 RCICTRGFCRCI 15
                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Best Local Similarity
   PIR; A59089; A59089.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=4931420D14Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                        23
65
74
66
68
38
76 AA;
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CONFLICT
SEQUENCE
                                                                                                                                     DISULFID
                                                                                        PROPEP
PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                RESULT 2
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3 CRCICTRGFCRCICTR 18

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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
THE FANTOM CONSORTIUM.
The RAINFOM CONSORTIUM.
The RAINFOM CONSORTIUM.
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573(2002).
[4]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUE=Testis; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carminci P., Hayashizaki Y.; Hiquehizaki Y.; Hiquehicaki Y.; Miquehicaki Y.; Miquehicaki Y.; Miquehicaki Y.; Miquehicaki Y.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 12, Last sequence update)
Mus musculus adult.male testis cDNA, RIKEN full-length enriched
library, clone:1700065105 product:hypothetical Cysteine-rich region
Containing protein, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
MEXEN FANTOM CONSOrtium;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CD-1; TISSUE=Testis;
STRAIN=CD-1; TISSUE=Testis;
Xu X., Bai X., Silvius D., Escalier D., McFarland L., Xu P.-X.;
Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF4653602; AA015675.1; --
MGD; MGI:1913992; 4931420D14Rik.
SEQUENCE 168 AA; 18957 MW; 8F30D3D27B9BF595 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 168;
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                                                                                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.9%; Score 59; DB 3 56.2%; Pred. No. 2.9;
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                                                                                                                                                                                                                                                                                                                                                                                                 Basic protein CKT1R3.
Name=4931420D14Rik; Synonyms=Ckt1r3;
                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                PRT;
81
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                                                                                                                                                                                                    PRELIMINARY;
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Hypothetical
SEQUENCE 17
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SEQUENCE FROM N.A.

Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

A Adachi J., Aizawa K., Akahira S., Fukuda S., Fukunishi Y., Furuno M.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Kato H.,

A Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

RA Soqabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

RA Fejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

RA Muramatsu M., Hayashizaki Y.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Testis;

MEDLINE=20530913; Pubmed=1107661; DOI=10.1101/gr.152600;

MEDLINE=20530913; Pubmed=1107661; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Tashiro H., Itoh M., Ashiwan J., Nakamura S., Hazama M., Nishine T., Harada A., Sami N., Ishii Y., Matsumcto H., Sakaguchi S., Ikeshiwangi K., Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramateu M., Inoue Y., Kira A., Hayashizaki Y., Warshiki M., Inoue Y., Kira A., Hayashizaki Y., Rikki integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
                                            MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Muramatisation and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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STRAIN=CS7BL/6J; TISSUE=Testis;
MEDLINE=9279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayadhizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Q9D4K2;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OT-2002 (TrEMBLrel. 22, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4931420D14 product:hypothetical Cysteine-rich region Name=4931420D14R1k;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Hypothetical protein.
SEQUENCE 168 AA; 18931 MW; 7A2BD279612A5E94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.9%; Score 59; DB 2; 56.2%; Pred. No. 2.9;
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                       STRAIN=C57BL/6J; TISSUE=Testis
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Best Local Similarity
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C STRANN-C57BL/6J; TISSUB=Testis;
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayateu N., Hiramoto K., Hiraoka T., Hori F.,
A managaki T., Hara A., Hayateu N., Hiramoto K., Hiraoka T., Hori F.,
A Kawai J., Kolima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Sakai K.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sogbe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Buhuntted (JUL.2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                    JAMEST CONSORTIUM,
The FANTOM CONSORTIUM,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
An 770 full-length CDNAS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRANNE-2059LL/6J; TISSUE=Testis;
STRANNE-2049374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                              RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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173 AA; 19581 MW; 147B6F155AC29FDF CRC64;
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STRAIN=C57BL/6J; TISSUE=Testis;
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552 GSYRCICARGFSGPLCT 568
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PRINTS; PR00907; THRMBOMODULN.
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58.8%;
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                                                      PRELIMINARY;
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                                                                                                                                                                                                                                    NCBI_TaxID=7719;
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SEQUENCE 937
                                                                                                                                                               Name=Ci-metal;
                                                                                           01-JUN-2001
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Q9BLJ1;
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STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; PubMed=12218036;
MEDLINE=22206494; PubMed=12218036;
DOI=10.1128/JB.184.19.5479-5490.2002;
Fleischmann R.D., Alland D., Bisen J.A., Carpenter L., White O., Peterson J.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H., Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M., Gill J., Mikula A., Bishai W., Jacobs W.R. Jr., Venter J.C.,
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                                                                                                                                                                               MEDLINE=21129048; PubMed=11435398; DOI=10.1101/gr.GR-1617R; Mayer K., Murphy G., Tarchini R., Wambutt R., Volckaert G., Pohl T., Duesterhoeft A., Stiekema W., Entian K.D., Terryn N., Lemcke K., Haase D., Hall C.R., van Dodeweerd A.M., Tingey S.V., Mewes H.W., Bavan M., Bancroft I.; "Conservation of microstructure bewtween a sequenced region of the genome of rice and multiple segments of the genome of Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                        Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Pred. No. 5.8;
3; Mismatches 2; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                                                                                                50.9%; Score 59; DB 2; Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR; MT3454; -.
Hypothetical protein.
SEOUENCE 163 Aa; 18621 MW; BSE62AB951B2AC3C CRC64;
                                                                                                                                                                                                                                                                                                                                          EMBL; AJ307662; CAC39030.1; -.
Gramene: Q949G1; -.
Hypothetical protein.
SEQUENCE 274 AA; 28657 MW; AB547D9BD5470AE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Hypothetical protein CISERIPDM. Name=CISERIPDM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laboratory strains.";
J. Bacteriol. 184:5479-5490(2002).
EMBL; AE000516; AAK47795.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3,
                                                                                                                                                                                                                                                                                                                            Genome Res. 11:1167-1174(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 CRHVCTRSGYCRLVC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 RCCCHRCCCRCRATR 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, Hypothetical protein. OrderedLocusNames=WT3454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CRCICTR-GFCRCIC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 RCICTRGFCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 60.00
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 66.7
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                 NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                           thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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SEQUENCE FROM N.A.
MEDLINE=9901743; PubMed=9804551; DOI=10.1126/science.282.5391.1126;
Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L.,
Koonin E.V., Shallom S., Mason T., Yu K., Fujii C., Pederson J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
                                                                                                                                                                                                                                                                                               Nakayama A., Satou Y., Satoh N.;
"Isolation and characterization of genes that are expressed during Ciona intestinalism metamorphosis.";
Dev. Genes Evol. 211:184-189(2001).
EMBL; AB041857; BAB40596.1; -.
HSSP; P00743; ICCF.
                                                                                                                   Ciona intestinalis.
Eukaryota, Metazoa, Chordata, Urochordata, Ascidiacea, Enterogona,
Phlebobranchia, Cionidae, Ciona.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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NCBL_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 56; DB 2; Length 937; Pred. No. 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                       GO, GO: 0005509; C: membrane; IEA.
GO, GO: 0005509; F: calcium ion binding; IEA.
GO; GO: 0004888; F: transmembrane receptor activity; IEA.
GO; GO: 0007596; P: blood coagulation; IEA.
InterPro; IPR000152; Asx hydroxyl S.
InterPro; IPR00042; EGF 2.
InterPro; IPR00181; EGF 2.
InterPro; IPR00181; EGF 1.
InterPro; IPR001212; Somatomedin B.
InterPro; IPR001212; Somatomedin B.
InterPro; IPR00181; Thrmbomoduln.
Pfam; PF00008; EGF 4.
Pfam; PF00008; EGF 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              937 AA; 101043 MW; 8C67830C8E391D07 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein PFB0950w.
                 01-JTN-2001 (TrEMBLrel. 17, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
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PROSITE; PS00010; ASX HYDROXXL; 14.

PROSITE; PS01186; EGF 1; 19.

PROSITE; PS01186; EGF 2; 19.

PROSITE; PS01187; EGF 3; 19.

PROSITE; PS01187; EGF 3; 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum (isolate 3D7).
Created)
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Gaps

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A Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Elkins T., Engels R., Wand S., Nielsen C.B., Butler J., Endrizzi M., Oui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., A Kothe G.O., Jedd G., Mewses W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., A Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B., The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 0:0-0(2003).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                            Neurospora crassa.
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
NCBI_TaxID=5141,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.6%; Score 54; DB 2; Length 991; 56.2%; Pred. No. 55; 7; Indels ive 0; Mismatches 7; Indels
                 Length 290;
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103024 MW; C51719B9F4D54A8E CRC64;
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                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
            46.6%; Score 54; DB 1;
40.7%; Pred. No. 19;
ive 2; Mismatches
                                                                                                                                                                                                                                                                               991
                                                                                                                                                       218 FARCFCINIMQCFCPRQGYKCECICRR 244
                                                                                                        2 FCRCICT-----RGF-CRCICTR 18
                                                                                                                                                                                                                                                                                                                              Created)
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EMBL; ABKKO1000029; EAA35288.1; -.
INTERPRO; IPRO06229; EGF like.
PROSITE; PS00122; EGF 1; 1.
PROSITE; PS01186; EGF 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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26,
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                                                           Conservative
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les 9; Conservative
                                                                                                                                                                                                                                                                             PRELIMINARY;
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01-MAR-2004 (TrEMBLrel.
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                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                               Predicted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           Name=NCU02165.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=OR74A;
         Query Match
Best Local Simi
Matches 11;
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Best Local 9
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                                                                                                                                                                                          MEDLINE=22255705; PubMed=12368864; DOI=10.1038/nature01097; Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W., Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K., Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.-S., Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.A., Pairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.;
Shen K., Jing J., Aston C., L'ai Z., Schwartz D.C., Pertea M., Salzberg S., Zhou L., Sutton G.C., Clayton R., White O., Smith H.O., Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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MEDLINE=94303173; PubMed=8030224;
Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
"The complete DNA sequence of Autographa californica nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
11-NOV-1995 (Rel. 34, Mar protein in LEF3-IAP2 intergenic region.
Autographa californica nuclear polyhedrosis virus (AcMMPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                 Fraser C.M., Barrell B.; "Genome sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001368; TNFR_c6.
PROSITE; P806652; TNFR_MGFR_1; UNKNOWN_1.
Wypotherical protein.
SEQUENCE 307 AA; 35537 MW; B95A3DB354D4BE71 CRC64;
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SEQUENCE 290 AA; 34408 MW; CA78BA9C8B5AB997 CRC64;
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60.0%; Pred. No. 18;
tive 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  falciparum.";
Nature 419:498-511(2002).
EMBL; AE001428; AAC71979.2; -.
PIR; E71602; E71602.
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                                                                                                                          Science 282:1126-1132(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polyhedrosis virus.";
Virology 202:586-605(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                      SEQUENCE FROM N.A.
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P41470;
                                                                                                      falciparum
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Y070_NPVAC

SEQUENCE Query Match

Matches

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Gaps

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Best Loc Matches

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RESULT 13 Q22048

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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein C04G6.10.
Name=C04G6.10; ORFNames=C04G6.10;
Caenorabaditis elegans.
Ebukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorabaditis.
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                                                                                                                                                                                                                                                                            "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45.7%; Score 53; DB 2; Length 166; 50.0%; Pred. No. 16; ive 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; U55854; AAK68158.1; -.
HSSP; P10969; 1WGT.
                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Bristol N2;
Anderson K., Chissoe S.;
"The sequence of C. elegans cosmid C04G6.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston R.; Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
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PROSITE; PSG0269; DEFENSIN; UNKNOWN_1.
PROSITE; PSG0022; EGF 1; UNKNOWN 1.
PROSITE; PSG1208; WHFC_1; UNKNOWN_1.
Hypothetical protein (F. 1971) MW; 9D9D130351BB50F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q18238;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
10-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein C27A2.5.
Name=C27A2.5; ORFNames=C27A2.5;
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WormPep; C04G6.10; CE27649.
                                                                                                                                                                                                                                STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
WormBase Consortium;
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN=Bristol N2;
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Wilson R.;
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                                                                                                                                                                         NCBI_TaxID=6239;
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Eukaryota, Metazoa; Nematoda; Chromadorea, Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
              Chesi M., Brents L.A., Ely S.A., Bais C., Mesri E.A., Robbiani D., Kuchl W.M., Bergsagel P.L.; Submitted (FRB-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AP238374; AAP9749.1; -. GO; GO:0004872; F:receptor activity; IEA.
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                                                                                                                                                                             DB 2; Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WormBase; WBGeneofol1313; TO1B7.8.
WormBase; TO1B7.8; CE03592.
InterPro; IPR001450; 4Fed5 ferredoxin.
InterPro; IPR006081; Defensin alpha.
InterPro; IPR006091; EGF_like.
InterPro; IPR006099; EGF_like.
InterPro; IPR001007; WWF.C.
PROSITE; PS001269; DEFENSIN; UNKNOWN 1.
PROSITE; PS001269; DEFENSIN; UNKNOWN 1.
PROSITE; PS01208; VWFC_1; UNKNOWN 1.
Hypothetical protein.
SEQUENCE 164 AA; 16499 MW; C002D48D36C9FCED CRC64;
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Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; Z66499; CAA91301.1; -.
PR; Y14272; T24272.
HSSP; P10969; IKTV.
IntAct; Q22048; -.
                                                                                                                                          174 AA; 17810 MW; BC9917E34470B9EA CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
101-NOV-1996 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein T01B7.8.
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Local Similarity 47.1%; Pred. No. 15;
les 8; Conservative 2; Mismatchae
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MEDLINE=99069613; PubMed=9851916;
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75 GLCVCVCV---CVCVCT 88
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Science 282:2012-2018(1998)
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Best Local Similarity
Matches 9; Conserv
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   SEQUENCE FROM N.A.
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SEQUENCE
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Gaps

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Caenorhabditis elegans.
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wormbep; C27A2.5; CE04105.

R GO; GO:0006952; P:defense response; IEA.

R GO; GO:0006952; P:defense response; IEA.

R InterPro; IPR001450; 4Fe45_ferredoxin.

R InterPro; IPR001007; VWF C.

R PROSITE; PS00198; 4Fe45_FERREDOXIN; UNKNOWN_1.

R PROSITE; PS01269; WFC_1; UNKNOWN_1.

R PROSITE; PS01208; WFC_1; UNKNOWN_1.
                                                                         SEQUENCE FROM N.A.
STRAINE-BYSIGED N2;
MEDLINE-99069613; PubMed-9851916;
WormBase Consortium;
"Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
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Best Local Similarity 50.0%; Pred. No. 18;
Matches 9; Conservative 0; Mismatches 9; Indels
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Wormbase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; US8760; AAK31463.1; -.
PIR; T15651; T15651.
HSSP: P10968; 2CWG.
                                                                                                                                                                                                                                                                                                                      Waterston R.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                             "The sequence of C. elegans cosmid C27A2."; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                Wilson R.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WormBase; WBGene00016153; C27A2.5.
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                                               NCBI TaxID=6239;
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81 GGCGCCCRPKCCCCCRR 98 8 셤

1 GPCRCICTRGFCRCICTR 18

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Gaps

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Total number of hits satisfying chosen parameters:

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Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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A Geneseq_16Deco4:*
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 geneseqp2000s:*
 geneseqp2001s:*
 geneseqp2001s:*

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:*

2105692 segs, 386760381 residues

Gapop 10.0 , Gapext 0.5

US-10-009-317A-33

Perfect score:

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Scoring table:

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12Y retro
111Y retr
Human ret
                   16Y retro
R9K retro
Rhesus th
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Theta def
Anti-vira
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Rhesus th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel theta defensin peptide with antimicrobial activity against bacteria, yeast, fungi, protozoa and viruses.
                   Ade33803
Ade33802
Ado8177
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Pred. No. 9.6e-06;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouellette AJ;
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               AAE33803
AAE33802
AD035381
AD08173
AD08179
AAE33805
AAE33805
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AAE33805
AAE3385
AAE33865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Theta defensin; antimicrobial; virus; helminth; disinfectant;
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100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Theta defensin SEQ ID NO: 31
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Best Local Similarity 100.
Matches 18; Conservative
 (REGC ) UNIV CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
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AAB35047;
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0XCCCCX8XX4XX8X1XX8X4X6X6X8X8X8X8X8X6X6X6X6X6X6X6X6X
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                                                                                                                        April 28, 2005, 13:57:35 ; Search time 122.5 Seconds (without alignments) 56.830 Million cell updates/sec
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Ad035241 R
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Query Match Length

Result No.

ABP53297

AAE3386 ADD95202 ADD35357 ADG70012 ADG35229 ADG35238 ADG35238 ADG35239 ADG3526 ADG3526

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ADN08176 ABP53299 AAE33804

ABP53294 AAE33801

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The present invention describes a method (M1) of using a first anti-viral peptide (I) comprising a theta-defensin peptide in an amphipathic alphabalical structure in a lipid environment for reducing the infectivity of a virus. (I) can have virunced and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-viral resistance. (I) can be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) protecting or reating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus in spread within a virally-infected subject (VS), reducing virus had from a VS, reducing percentage of VS in a VS, reducing virus shed from a VS, reducing percentage of VS in a VS, reducing the infectivity of a virus; and (c) rendering virus of virus infections virus particles in a population of viruses. (M1) is useful to request the infectivity of a virus in sheep, cartle, horses, waine, cats, fewl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is administered prior to or subsequent to the virus contacting the subject.

The anti-viral peptide is most preferably administered to a subject who is contacting the subject.

The anti-viral peptide is most preferably administered to a virus or a subject who is the virus of the virus where the virus contacting the virus meaning the virus of the virus or a variance of the virus where the virus or a variance of the virus where the virus or a variance of the variance of the variance of the virus where the virus or a variance of the variance of the variance of the virus or a variance of the variance of the virus or a variance of the vari
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                                                                                                                                                                                                                                                  Anti-viral; viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roller R, Mccray PB, Tack B;
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                                                                                                                                                                                                       Anti-viral theta defensin peptide RTD-3 SEQ ID NO:29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stinski M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 10; 65pp; English.
                                                 ABP53296 standard; peptide; 18 AA.
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01-AUG-2001; 2001US-0309368P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stapleton J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-674815/72.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200260468-A2.
                                                                                                                                                                                                                                                                                                                                                                     Macaca mulatta
                                                                                                                                                      13-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maury W,
                                                                                                    ABP53296;
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RESULT 2
                           ABP53296
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Monkey, Rhesus theta defensin, RTD-3, antimicrobial peptide, cyclic, antimicrobial, antiinflammatory, antibacterial, virucide, fungicide; food, contact lans solution, eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant, food preservative; bacterial infection, viral infection;

    .18
/note= "The peptide is cyclised by a covalent link
between these two residues"

                                                                                                                                                                     fungal infection; haemolytic activity
                                                                                                        Rhesus theta defensin peptide, RTD-3.
                                                                                                                                                                                                       Location/Qualifiers
                                                      Ā
GVCRCLCRRGVCRCLCRR 18
                                                      ADO35231 standard; peptide; 18
                                                                                                                                                                                                                                                                                                               30-APR-2003; 2003US-00427715.
                                                                                                                                                                                                                                                                                                                              30-APR-2002; 2002US-0377071P.
                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                  Selsted ME, Tran DQ;
                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-167945/16.
                                                                                                                                                                                                                                        Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                                                             US2004014669-A1
                                                                                                                                                                                       Macaca mulatta
                                                                                                                                                                                                         Key
Modified-site
                                                                                                                                                                                                                                                                                              22-JAN-2004.
                                                                                        15-JUL-2004
                                                                       AD035231;
                                              AD03523
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Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate object.

Example 1; SEQ ID NO 3; 46pp; English.

The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash colution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as the repetides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for the peptides of the production of such a patient suffering from the peptides are also useful for the peptides of the production of such an infection. The theta defensing have high antimicrobial activity and low haemolytic activity. The present sequence represents the rhesus monkey wild-type theta defensing RTD-3.

Sequence 18 AA;

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Gaps

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Indels

Mismatches

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Conservative

Local Similarity hes 18; Conserv

Matches

Score 112; DB 8; Length 18; Pred. No. 9.6e-06; 100.0%; Query Match Best Local Similarity

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1 GVCRCLCRRGVCRCLCRR 18

Gaps

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Length 18; Indels

Matches

ઠે 용 ADO35242

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Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial; antilnflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; alflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO35257. The theta defensin analogue is useful for reducing or inhibiting growth or survival
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of a microorganism in an environment capable of sustaining the growth or survival of the microorganism and is useful for reducing or inhibiting survival of the microorganism in an environment such as frond or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or ewe wash solution), an inanimate object comprising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as the repeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from bacterial, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                    Rhesus theta defensin analogue peptide aRTD-3-OH.
                          Score 112; DB 8;
Pred. No. 9.6e-06;
                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fungal infection; haemolytic activity.
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                                                                                                                  1 GVCRCLCRRGVCRCLCRR
                                                                                                                                                             GVCRCLCRRGVCRCLCRR
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                                                                       Conservative
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                       Query Match
Best Local Similarity
Matches 18; Conserv
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Disulfide-bond
Disulfide-bond
Modified-site
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                                                                                                                                                                                                                                                          AD03524
                                                                                                                                                                                                                                    RESULT
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                                                                                                                                                                                                                                                                                                                                                                                     Monkey; Rhesus theta defensin; RTD; antimicrobial peptide; antimicrobial; antiinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial inflection; viral infection; disinfectant; fungal infection; haemolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The peptides are also useful for treating a patient suffering from bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
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  0; Indels
                                                                                                                                                                                                                                                                                                                                             Rhesus theta defensin analogue peptide aRTD-3-NH.
Mismatches
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                                                                                                                                                                                                     ADO35242 standard; peptide; 18 AA.
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                                                                       GVCRCLCRRGVCRCLCRR 18
                                             1 GVCRCLCRRGVCRCLCRR 18
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                                                                                                                                                                                                                                                                                                (first entry)
Conservative
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5. .14
7. .12
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Disulfide-bond
Disulfide-bond
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18;
                                                                                                                                                                                                                                                                                                15-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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object.

Gaps

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0; Indels

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The present invention describes a method (M1) of using a first anti-viral peptide (1) comprising a theta-defensin peptide in an amphipathic alphabelic deficients in a substance of a virus a lipid environment for reducing the infectivity of a virus (1) can have virucide and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-viral resistence. (1) can be used for inhibiting the growth and proliferation of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent viral infection in a subject harbouring a latent virus, controlling virus spread within a virally-infected subject (VS) reducing virus latent virus of virus burden in a VS, reducing virus expread within a virally-infected subject (VS) reducing virus latent virus of virus burden in a VS, reducing virus and (c) rendering virus copulation regardless of viral infection status, or inducing latency in a VS; (b) reducing the infectivity of a virus; and (c) rendering virus contaminated tissue or fluid sample safe for use, or reducing the number of infectious virus particles in a population of viruses. (MI) is useful for reducing the infectivity of a virus in sheep, cattle, horses, as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-viral; viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
The peptides are also useful for treating a patient suffering from
                                           bacterial, viral, fungal or other infection. The theta defensins have high antimicrobial activity and low haemolytic activity. The present sequence represents a Rhesus theta defensin analogue peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-viral chimeric theta defensin peptide H/RTD-3 SEQ ID NO:31,
                                                                                                                                                                                            Score 107; DB 8; Length 18;
Pred. No. 3.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Roller R,
                                                                                                                                                                                                              100.0%; Pred. no.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 10; 65pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP53298 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                            GVCRCLCRRGVCRCLCR 18
                                                                                                                                                                                                                                                                                                1 GVCRCLCRRGVCRCLCR 17
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01-AUG-2001; 2001US-0309368P.
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                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 17; Conservative
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                                                                                                   sequence represents a
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                                                                                                                                                 Sequence 18 AA;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Monkey, Rhesus theta defensin, RTD; antimicrobial peptide; antimicrobial; antiinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.
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                                                                                                                                                                             Gaps
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                            sequence represents a Rhesus theta defensin analogue peptide.
                                                                                                                             Length 18;
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                                                                                                                          Score 112; DB 8;
Pred. No. 9.6e-06;
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                                                                                                                             Query Match
Best Local Similarity
Matches 18; Conserv
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Disulfide-bond
Disulfide-bond
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                                                                               Sequence 18 AA;
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22-JAN-2004.

Synthetic.

Selsted ME,

object.

15-JUL-2004

AD035243;

RESULT 6

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Tack B;

Mccray PB,

18

(first entry)

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Anti-viral; viral infection; theta-defensin; lipid environment; amphipathic alpha-helical structure; virucide; anti-HIV; immunisation; viral growth inhibitor; viral proliferation inhibitor.
                                                                                                                                                                       Anti-viral theta defensin peptide RTD-1 SEQ ID NO:30.
                                                                                    ABP53297 standard; peptide; 18 AA
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                                                                                                                                                                                                                                                             Macaca mulatta.
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                                                                                                                                                                                                                                                                            Synthetic.
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administered to a patient who is immunosuppressed or to a subject who is not infected with the virus, where the first anti-viral peptide is administered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is most preferably administered to a subject who is chronically, latently infected with the virus. The present sequence represents a chimeric human thesus monkey theta defensin anti-viral peptide, which is given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides theta defensin peptides and analogues which have antinicrobial activity. They can be used in the treatment of bacterial, viral, fungal, protozoan and helminthic infections, in disinfectants and as food preservatives
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                  lefensin; antimicrobial; cyclic; bacterium; fungus; protozoan; helminth; disinfectant; food preservative; analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel theta defensin peptide with antimicrobial activity against
                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .18
'note= "peptide bond cyclises the molecule"
                                                                                                                                                           Length 18;
                                                                                                                                                                                      1; Indels
                                                                                                                                                        Score 102; DB 5;
Pred. No. 0.00012;
2; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bacteria, yeast, fungi, protozoa and viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouellette AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 4; 110pp; English
                                                                                                                                                                                      2;
                                                                                                                                                                                                                  18
                                                                                                                                                                                                                                                                                                                   AAB35030 standard; peptide; 18
                                                                                                                                                                                                                                 GICRCLCRRGVCRCICGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yuan J,
                                                                                                                                                          91.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-MAY-2000; 2000WO-US012842
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-00309487
                                                                                                                                                                                                                  GVCRCLCRRGVCRCLCRR
                                                                                                                                                                                                                                                                                                                                                                                                       Theta defensin SEQ ID NO: 1.
                                                                                                                                         Ouery Match
Best Local Similarity 83.3.
Best Local Similarity 83.3.
Local Similarity 83.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . . . 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-031853/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Theta defensin;
                                                                                                                              Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200068265-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                           27-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-links
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Selsted ME,
                                                                                                   invention
                                                                                                                                                                                                                                                                                                                                               AAB35030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  virus;
                                                                                                                                                                                                                                                                                                       AAB35030
                                                                                                                                                                                                                                                                                        RESULT
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ä Tack

Mccray PB,

Roller R,

Stinski M,

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the present interition describes a mechanic viri, or using a filter anti-virial peptide (I) comprising a theta-defensin peptide in an amphipathic alphabalical structure in a lipid environment for reducing the infectivity of a virus (I) can have viruside and anti-HIV activities, and can be used to reduce virus growth, infectivity burden, shed, and development of anti-viral resistance. (I) can be used for inhibiting the growth and complete states of a virus and so can be used for; (a) protecting or treating subject from a viral infection, preventing recurrent virus infection in a subject harbouring a latent virus, controlling virus shed from a VS, reducing virus burden in a Spread within a virally-infected subject (VS), reducing virus burden in a VS, reducing virus for a viral infection status, or inducing virus contaminated tissue or fluid sample safe for use, or reducing the number of infections virus particles in a population of viruses. (MI) is useful or reducing the infectivity of a virus; and (c) rendering virus as for reducing the infectivity of a virus in sheep, cattle, horses, swine, cats, fowl and humans e.g. an enveloped virus infecting humans such as human immunodeficiency virus (HIV). Preferably, the anti-viral peptide is administered to a patient who is immunosuppressed or to a subject who is caministered prior to or subsequent to the virus contacting the subject. The anti-viral peptide is amontal virus contacting the subject. The anti-viral peptide is an enveloped virus in the virus contacting the subject. The anti-viral peptide is an enveloped virus in the virus on a subject who is a contacting the auti-viral peptide is an enveloped virus contacting the subject. The anti-viral peptide is an enveloped virus contacting the subject. The anti-viral peptide is an enveloped virus contacting the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                        present invention describes a method (M1) of using a first anti-viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ically, latently or acutely infected with the virus. The present represents a rhesus monkey theta defensin anti-viral peptide,
New method of using a first anti-viral peptide comprising a Theta-defensin peptide in an amphipathic Alpha-helical structure in a lipid environment for reducing the infectivity of a virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Pred. No. 0.00024;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                       Disclosure; Page 10; 65pp; English.
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83.3%;
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Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 18 AA;
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Gaps

; 0

2; Indels

1; Mismatches

1 GVCRCLCRRGVCRCLCRR 18

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Score 99; DB 4; Length 18; Pred. No. 0.00024;

88.4%;

Best Local Similarity 83.3 Matches 15; Conservative

Query Match

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New conjugate of transport mediator and active agent, useful for treating prokaryotic infections, especially by neutralizing antibiotic resistance
                         bacterial infection; human pathogen; holin; defensin; peptide nucleic acid; PNA; penicillin; tetracycline; ampicillin; kanamycin; antibiotic; antibacterial; antibiotic-resistance gene; cyclic.
                                                                                                                                       1. .18
/note= "Residue 1 and residue 18 bond to form a cyclic
                                                                                                                                                                                                                                                                                                                                                                                                   Braun K, Braun I, Debus J, Pipkorn R,
                                                                                                                                                                                                                                                                                                                                                                     (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM
                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 10; 34pp; German.
                                                                                                                                                                                                                                                                                                                                        18-JAN-2002; 2002DE-01001862.
                                                                                                                                                                                                                                                                                                          17-JAN-2003; 2003WO-DE000124
Cyclic defensin fragment.
                                                                                                                                                                  moiety"
3. .16
5. .14
7. .12
                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-689464/65
                                                                                                                       Key
Misc-difference
                                                                                                                                                                                Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                                                                                                                                                                              WO2003059392-A2
                                                                                        Unidentified
                                                                                                                                                                                                                                                                              24-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the invention are useful for preventing retroviral infections in cells susceptible to bacterial or viral infections, or treating patients having infections such as HIV (human immunodeficiency virus), sexually transmitted diseases, bacterial vaginosis or ophthalmic infections. The retrocyclin-mediated killing is useful for modelling and screening novel sequence is rheaus monkey theta defensin, RIDI peptide. This sequence is used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel retrocyclin peptides. Peptides and methods
                                                                                                                                                                                                                                              Retrocyclin; infection; sexually transmitted disease; gene therapy; HIV; human immunodeficiency virus; bacterial vaginosis; ophthalmic infection; antibiotic modelling; antimicrobial; rhesus monkey; theta defensin 1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infections in cells susceptible to bacterial or viral infections or treating patients having the infections, such as HIV, sexually
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          isolated retrocyclin peptide, useful for preventing retroviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.00024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 99; DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 0.00
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŢB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hong
                                                                                                                        AAE33866 standard; peptide; 18 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 3C; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cole AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmitted diseases, vaginosis.
                   GVCRCLCRRGVCRCLCRR 18
                                  GFCRCLCRRGVCRCICTR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                   18-APR-2002; 2002WO-US012353.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-APR-2001; 2001US-0284855P
                                                                                                                                                                                                                 Macaca mulatta RTD1 peptide.
                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 83.3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Waring AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-103387/09.
                                                                                                                                                                                                                                                                                                                          Macaca mulatta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18 AA;
                                                                                                                                                                                                                                                                                                                                                        WO200285401-A1.
                                                                                                                                                                                     16-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                     31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RI,
                                                                                                                                                        AAE33866;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lehrer
                                                                                            RESULT
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Waldeck W;

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This invention describes a novel conjugate for treating prokaryotic confections which comprises a transport mediator for passage through the prokaryotic cell membrane and a compound, directed against a prokaryote and intended for introduction into it. The prokaryote is a bacterium, especially one pathogenic in humans. The transport mediator is preferably captured or protein, especially a phage-holin protein, its active fragment or variant or a defensin. The introduced compound is a peptide or uncleic acid (PNA) that inhibits a gene, especially one implicated in resistance to penicillin, tetracycline, ampicillin or kanamycin. The conjugate has the structure transport mediator spacer-PNA where the spacer is the structure transport mediator through a cids and the spacer is linked to the transport mediator through a cleavable disulfide bridge. The conjugates are administered together with an antibiotic, by parenteral, transdormal or subcutaneous routes. The products of the invention have antibacterial activity and are used, especially in combination with antibacterial activity and are used, especially bacterial, infections, especially where the pathogen is pathogen is cantibiotic resistance gene. Where the PNA is directed against the antibiotic resistance gene. Where the PNA is directed against constitute to co-administered antibiotics and the bacterial infections, especially in cases where normally they would be ineffective. This sequence represents a cyclic defensin fragment described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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0
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Pred. No. 0.00024;
1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disclosure of the invention.
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nes 15; Conservative
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RESULT 12

ADD95202 standard; peptide; 18 AA.

RESULT 11 ADD95202 (first entry)

29-JAN-2004

X Z Z X

ADD95202;

18 18

1 GVCRCLCRRGVCRCLCRR GVCRCICTRGFCRCLCRR

ઠે 셤 Gerdes

Brunner N,

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for preparing a composition for treatment and/or prevention of bacteraemia for binding bacterial products such as lipopolysaccharide (LPS) and/or lipteichonic acid (LTA), or for treatment and/or prevention of septic shock. RTD-1, isolated from immune cells of rhesus monkeys, has antibacterial, fungicide, virudide, immunomodulator and anticoagulant activity. RTD-1 inhibits microbial cell-wall biosynthesis and also binds to LPS and LTA. RTD-1 is useful for treatment and prevention of severe infections caused by Gram-positive or negative bacteria and yeasts, or by viruses. RTD-1 combines four advantageous properties: a direct antimicrobial action, neutralisation of bacterial products (by binding),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes the novel use of rhesus theta defensin-1 (RTD-1)
                                                                                                                                                                                                                                                                                                                                                                                                Use of rhesus theta defensin-1 for treating or preventing bacteremia and septic shock, also for binding bacterial products and as immunomodulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunomodulation (reducing release of proinflammatory cytokines but increasing release of regulatory factors) and anticoagulant action, so provides a better and simpler treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monkey, Rhesus theta defensin, RTD-1; antimicrobial peptide; cyclic; antimicrobial; antinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection;

    .18
/note= "The peptide is cyclised by a covalent link
between these two residues"

  microbial cell-wall biosynthesis; immunomodulation; anticoagulant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 99; DB 8; Length 18; Pred. No. 0.00024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fungal infection; haemolytic activity
                                                                                                                                                                                                                                                                                                             Labischinski H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rhesus theta defensin peptide, RTD-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; SEQ ID NO 1; 28pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                           30-MAY-2003; 2003WO-EP005694.
                                                                                                                                                                                                                       13-JUN-2002; 2002DE-01026216.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GVCRCLCRRGVCRCLCRR
                                                                                                                                                                                                                                                                  (FARB ) BAYER HEALTHCARE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Conservative
                                                                                                                                                                                                                                                                                                             C, Newton B,
                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-071500/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         septic shock, also
and anticoagulant.
                                                                                         WO2003105883-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18 AA;
                                             Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Macaca mulatta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUL-2004
                                                                                                                                  24-DEC-2003
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                                                                                                                                                                                                                                                                                                             Ladel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel ophthalmic solution comprising a prostaglandin of the F-series and an antimicrobial peptide. A solution of the invention has hypotensive and ophthalmological activity. The solution is useful for the treatment of increased intraocular pressure, such as caused by glaucoma and for the reduction of ocular hypertension. The prostaglandin and the antimicrobial peptide work synergistically, to provide beneficial reduction in the incidence of irritant and toxic side effects such as hyperaemia, irritation and inflammation of conjunctiva, ocular cell dysplasia, iridial melanocyte hyperplasia, and hyperpigmentation, associated with the prior art prostaglandin compositions. The present sequence represents an antimicrobial peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rhesus theta defensin-1; RTD-1; bacteraemia; lipopolysaccharide; LPS; lipteichonic acid; LTA; septic shock; antibacterial; fungicide; virucide; immunomodulator; anticoagulant activity;
                                                                                                                                                                                             antimicrobial; ophthalmic; prostaglandin; hypotensive; ophthalmological; intracoular presente; ocular hypetension; hyperaemia; irritation; inflammation; coular cell dysplasia; irritation; inflammation; organization; hyperplasia; hyperpigmentation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ophthalmic solution useful for the treatment of increased intraocular pressure comprises a prostaglandin of the F-series and an antimicrobial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 0.00024;
Pred. Lanches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rhesus theta-defensin-1 (RTD-1) peptide.
                                                                                                                                                  Antimicrobial peptide theta-defensin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 11; 11pp; English.
                    ADD35357 standard; peptide; 18 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-MAR-2002; 2002US-0367071P.
                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAR-2003; 2003WO-US008935
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                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Maxey KM, Johnson J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CAYM-) CAYMAN CHEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-011506/01.
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                                                                                                                                                                                                                                                                                                                                                    WO2003079997-A2
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                                                                                                         15-JAN-2004
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                                                                ADD35357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monkey, Rhesus theta defensin, RTD; antimicrobial peptide; antimicrobial; antiinflammatory; antibacterial; virucide; fungicide; food; contact lens solution; eye wash solution; inflammatory response; microbicidal inhibition; microbistatic growth inhibition; disinfectant; food preservative; bacterial infection; viral infection; disinfectant; fungal infection; haemolytic activity.
                                                                                                                                                                                                                                                                                                                                                                                                       Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.4%; Score 99; DB 8; Length 18; 83.3%; Pred. No. 0.00024; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhesus theta defensin analogue peptide aRTD-1-OH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 1; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADO35238 standard; peptide; 18 AA.
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                                                                                                                                                                              30-APR-2003; 2003US-00427715
                                                                                                                                                                                                                             30-APR-2002; 2002US-0377071P
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Best Local Similarity 83.3
Matches 15; Conservative
                                                                                                                                                                                                                                                                       (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                   Tran DQ
                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-167945/16.
Disulfide-bond
Disulfide-bond
Disulfide-bond
                                                                                        US2004014669-A1
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Synthetic.
                                                                                                                                    22-JAN-2004.
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The invention relates to a theta defensin analogue defined by formulae detailed in the claims or appearing as ADO35239-ADO3527. The theta defensin analogue is useful for reducing or inhibiting growth or survival of a microorganism in an environment capable of sustaining the growth or survival of a microorganism and is useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, a solution (e.g., contact lens solution, or eye wash solution), an inanimate object compatising surface, or a mammal. The peptides are also useful for decreasing inflammatory response and for microbicidal inhibition of survival of microorganism as well as microbistatic inhibition of growth. Thus the peptides are useful as therapeutic agents, disinfectants, food preservatives, or medicaments. The peptides are also useful for treating a patient suffering from the peptides are also useful for treating a patient suffering from the peptides are also useful for theating a patient suffering from the peptides are also useful for the analogue peptide. Suffering from the peptides are also useful for the analogue peptide. Suffering from the peptides are also useful for the analogue peptide. Suffering from the analogue represents a Rhesus theta defensin analogue peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel theta defensin analog useful for reducing or inhibiting growth or survival of a microorganism in an environment such as food or food product, contact lens solution, or eye wash solution, an inanimate
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Location/Qualifiers
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Best Local Similarity
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                                     Disulfide-bond
Disulfide-bond
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                                                                                                                                                Modified-site
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Best Local Similarity 83.3
Matches 15; Conservative
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US-09-309-487-1
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LENGTH: 18
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Sequence 1, Appli
                                                                                                                 April 28, 2005, 14:12:37; Search time 30 Seconds (without alignments) 44:789 Million cell updates/sec
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Sequence 1,
Sequence 2,
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Sequence 9
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Sequence 1
Sequence 2
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-309-487-1
US-09-367-808-1
US-09-309-408-9
US-10-141-645-1
US-10-141-645-3
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US-10-141-645-3
US-10-141-645-4
US-10-141-645-6
US-10-141-645-8
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-09-309-487-21
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-10-141-645-73
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Maximum Match 100%
Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
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112
1 GVCRCLCRRGVCRCLCRR 18
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Maximum DB seq length: 200000000
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45, Appl
121, App
65, Appl
69, Appl
32502, A
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APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Yan, Jun
APPLICANT: Ovellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REFERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309_487
CURRENT FILING DATE: 1999-05-10
WUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.0
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US-09-567-808-1

i Sequence 1, Application US/09967808

Sequence 1, Application US/09967808

GENERAL INFORMATION:
APPLICANT: Tang, Yi-Quan
APPLICANT: Tang, Yi-Quan
APPLICANT: Vuan, Jun
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Ammicrobial Theta Defensins and Methods of Using
TITLE OF INVENTION: Same
FILE REFERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/967,808
FILE REPERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
PRIOR PILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTHARE: Patentin Ver. 2.0
SSEQ ID NO 1
LENGTH: 18
                                                                                                                                                  33, Appl
12, Appl
4, Appli
2, Appli
4, Appli
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                                                                                                                 Sequence 3
Sequence 4
Sequence 5
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Pred. No. 9.3e-06;
1; Mismatches 2; Indele
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US-10-042-872-1

US-09-510-238A-286

US-09-309-487-20

US-09-967-808-20

US-10-141-645-45

US-10-141-645-45

US-10-141-645-65

US-10-141-645-69

US-10-141-645-69

US-10-141-645-69

US-09-252-991A-32502

US-09-270-767-40304

US-09-270-767-40304

US-09-270-767-5520

US-10-141-645-33

US-10-141-645-33

US-10-141-645-33

US-08-899-811-4

US-08-899-811-4

US-08-999-811-4

US-08-999-811-4

US-08-999-811-4
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                                                                                                                                                                                      FERERAL INFORMATION:

APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
TITLE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR PRICATION NUMBER: 100-04-18
PRIOR PLICATION NUMBER: 100-04-18
PRIOR PLICATION NUMBER: Unassigned
PRIOR APPLICATION NUMBER: UNASSIGNED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-141-645-2
Sequence Application US/10141645
Patent No. 6713078
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan Waring
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REPERENCE: UCLA-001CIP
CURRENT FILING DATE: 2002-05-06
PRIOR PILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR APPLICATION NUMBER: 00-104-18
PRIOR APPLICATION NUMBER: 00-284,855
SOFTWARE: PASSE OF MINGER: 128
SOFTWARE: PASSE OF MINGER: 108
SOFTWARE: PASSE OF WINGOWS VERSION 4.0
SSQ ID NO 2
LENGTH: 18
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                                                                                                                                         ; Sequence 1, Application US/10141645; Patent No. 6713078
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ORGANISM: Artificial Sequence
3 GFCRCLCRRGVCRCIC 18
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Best Local Similarity 66.73
Matches 12; Conservative
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US-10-141-645-1
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US-09-967-808-9
; Sequence 9, Application US/09967808
; Patent No. 614727
; GENERAL INFORMATION:
; APPLICANT: Selsted, Michael E.
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Tang, Yi-Quan
; APPLICANT: Outliette, Andre J.
; TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using
; TITLE OF INVENTION: Same
; FILE REPERROR: P-UC 3095
; CURRENT APPLICATION NUMBER: US/09/967,808
; CURRENT FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 18
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APPLICANT: Tangy 'Yi-Quan
APPLICANT: Tangy 'Yi-Quan
APPLICANT: Yuan, Jun
APPLICANT: Yuan, Jun
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
FILE REPERBUCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT FILING DAFE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 84.8%; Score 95; DB 3; Length 18; Best Local Similarity 87.5%; Pred. No. 2.7e-05; Matches 14; Conservative 1; Mismatches 1; Indels
                                                                                                                 Length 18;
                                                                                                                 Query Match 88.4%; Score 99; DB 4; Length 18; Best Local Similarity 83.3%; Pred. No. 9.3e-06; Matches 15; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           US-09-309-487-9; Sequence 9; Application US/09309487; Patent No. 633518; Eatent INFORMATION:
                                                                                                                                                                                                                                                                    1 GFCRCLCRRGVCRCICTR 18
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US-09-309-487-9
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US-09-967-808-9
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-967-808-1
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Pred. No. 0.00018;
3; Mismatches 3;
                                                                                            APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral a
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001GTP
CURRENT APPLICATION UNMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
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PRIOR APPLICATION NUMBER: 60/284,855

PRIOR FILING DATE: 2001-04-18

PRIOR APPLICATION NUMBER: Unassigned

PRIOR PILING DATE: 2002-04-18

NUMBER OF SEQ ID NOS: 125

SOFTWARE: FastSEQ for Windows Version 4.0

EDNOTH: 18

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PRIOR FILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
SECOND ID NOS: 18
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APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral
TITLE OF INVENTION: Antimicrobial Peptides
FILE REPERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: synthetic variant US-10-141-645-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 6, Application US/10141645; Patent No. 6713078; GENERAL INFORMATION: APPLICANT: Robert Lehrer
                          ; Sequence 5; Application US/10141645; Patent No. 6713078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 66.7%;
Matches 12; Conservative
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APPLICANT:
APPLICANT:
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                                         GENERAL INPORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
ITILE OF INVENTION: Retrocyclins - Antiviral and
ITILE OF INVENTION: Antimicrobial Peptides
FILE REPERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alan waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REPERENCE: UCLA-001CIP
CURRENT FILING DATE: 2002-05-06
PRIOR PPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR PLICATION NUMBER: Unassigned
PRIOR PLICATION NUMBER: Unassigned
PRIOR PLICATION NUMBER: 1036-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/284,855
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: Unassigned
PRIOR FILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
OTHER INFORMATION: synthetic variant
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Sequence 3, Application US/10141645 Patent No. 6713078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10141645
Patent No. 6713078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT CRGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 66.74
Matches 12; Conservative
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LENGTH: 18
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LENGTH: 18
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                                                                                                          Sequence 8, Application US/10141645;
Patent No. 6713078;
GENERAL INFORMATION:
APPLICANT: Robert Lehrer;
APPLICANT: Alan Waxing
APPLICANT: Alan Waxing
APPLICANT: Alan Waxing
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP;
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT APPLICATION NUMBER: 2002-05-06
PRIOR APPLICATION NUMBER: 2002-06-06
PRIOR PILING DATE: 2001-04-18
PRIOR FILING DATE: 2001-04-18
NUMBER OF SEQ ID NOS: 125
SEQ ID NOS
SEQ ID NOS: 128

LEASTHARE: FASTESEQ FOR Windows Version 4.0
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Patent No. 6713078

GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Alexander Cole
APPLICANT: Alexander Cole
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFRENCE: UCLA-001CIP
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: US/85

PRIOR FILING DATE: 2001-04-18

PRIOR FILING DATE: 2001-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 77; DB 4;
Pred. No. 0.0033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: synthetic variant US-10-141-645-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: synthetic variant US-10-141-645-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 68.8%;
Best Local Similarity 55.6%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GVCRCLCRRGVCRCLCRR
  1 RCICTRGFCRCLGRR 15
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Best Local Similarity 55.69
Matches 10, Conservative
                                                                      RESULT 13
US-10-141-645-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-141-645-9
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71.4%; Score 80, DB 4; Length 18;
Best Local Similarity 80.0%; Pred. No. 0.0015;
Matches 12; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 75.9%; Score 85; DB 4; Length 18; Best Local Similarity 61.1%; Pred. No. 0.00039; Matches 11; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                               APPLICANT: Robert Lehrer
APPLICANT: Alan Waring
APPLICANT: Alan Waring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Retrocyclins - Antiviral and
TITLE OF INVENTION: Antimicrobial Peptides
TITLE OF INVENTION: Antimicrobial Peptides
FILE REFERENCE: UCLA-001CIP
CURRENT APPLICATION NUMBER: US/10/141,645
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: Unassigned
PRIOR APPLICATION NUMBER: Unassigned
PRIOR PILING DATE: 2002-04-18
NUMBER OF SEQ ID NOS: 125
SOFTWARE: FRSESEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-0917-340-53

US-0917-340-53

Sequence 53, Application US/09917340

Patent No. 6696238

GENERAL INPORMATION:
APPLICANT: Murphy, Christopher J.
APPLICANT: McAnlity, Jonathan F.
APPLICANT: Reid, Ted W.
TITLE OF INVENTION: Transplant Media
FILE REFERENCE: TPLANT-06466
CURRENT PELLING DATE: 2001-07-29
FRIOR FILING DATE: 2000-07-28
PRIOR FILING DATE: 2000-11-17
SPRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 96

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 53
LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: synthetic variant US-10-141-645-7
                                                                                                                                             Sequence 7, Application US/10141645
Patent No. 6713078
GENERAL INFORMATION:
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US-09-917-340-53
                                                                                                     RESULT 11
US-10-141-645-7
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RESULT 15
US-09-309-487-22
Sequence 22, Application US/09309487
SEPERAL INPORTATION: Andre J.
APPLICANT: Tang, Yi-Quan
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same
CURRENT APPLICATION NUMBER: US/09/309,487
CURRENT PILING DATE: 1999-05-10
SOURRENT PILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 31
SOFTWARE: PREFERE PATENTIN Ver. 2.0
SEQ ID NO 22
ILENGTH: 92
ILENGTH: 93
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                                                                                                                                                                                                                 April 28, 2005, 14:13:43 ; Search time 91 Seconds (without alignments) 65.889 Million cell updates/sec
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6/ptodata/1/pubpaa/USO9C_PUBCOMB.pep: *
6/ptodata/1/pubpaa/USO9 NEW PUB.pep: *
6/ptodata/1/pubpaa/USO9 NEW PUB.pep: *
6/ptodata/1/pubpaa/USIOB PUBCOMB.pep: *
6/ptodata/1/pubpaa/USIOC_PUBCOMB.pep: *
6/ptodata/1/pubpaa/USIOC_PUBCOMB.pep: *
6/ptodata/1/pubpaa/USIOC_PUBCOMB.pep: *
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1: /cgn2 6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2 6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
2: /cgn2 6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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5: /cgn2 6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
6: /cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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8: /cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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13: /cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
14: /cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
15: /cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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18: /cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
19: /cgn2 6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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112
1 GVCRCLCRRGVCRCLCRR 18
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Description | Sequence 29, Appl | | Sequence 15, Appl | 16, | 29, | Sequence 17, Appl | Sequence 31, Appl | 31, | 30, | Sequence 1, Appli | Sequence 1, Appli | Sequence 12, Appl | 13, |
|-------------------------------|-------------------|-----------------|-------------------|------------------|------------------|-------------------|-------------------|------------------|------------------|-------------------|-------------------|-------------------|------------------|
| QI QI | US-10-060-102-29 | US-10-427-715-3 | US-10-427-715-15 | US-10-427-715-16 | US-10-721-839-29 | US-10-427-715-17 | US-10-060-102-31 | US-10-721-839-31 | US-10-060-102-30 | US-10-313-994-1 | US-10-427-715-1 | US-10-427-715-12 | US-10-427-715-13 |
| | 14 | 15 | 15 | 15 | 12 | 15 | 14 | 15 | 14 | 14 | 15 | 15 | 12 |
| % Query Match Length DB | 18 | 18 | 18 | 18 | 18 | 18 | 18 | 18 | 18 | 18 | 18 | 18 | 18 |
| % Query Match | 100.0 | 100.0 | 100.0 | 100.0 | 100.0 | 95.5 | 91.1 | 91.1 | 88.4 | 88.4 | 88.4 | 88.4 | 88.4 |
| Score | 112 | 112 | 112 | 112 | . 112 | 107 | 102 | 102 | 66 | 66 | 66 | 66 | 66 |
| Result No. | н | 8 | e | 4 | Ŋ | 9 | 7 | 8 | 6 | 10 | 11 | 12 | . 13 |

| Sequence 30, Appl | Sequence 30, Appl | 6 | 27 | Ä | 7 | 32 | 'n | Sequence 3, Appli | 4, | 18 | 32 | 'n | ý | 28 | ď | Sequence 14, Appl | 23 | 29 | 28 | 7 | 28 | 19, | 20, | 31 | 53, 7 | 53 | 67 | 8, | o, | Sequence 37, Appl | 38, |
|--------------------|--------------------|---|-------|-------------------|-------|--------------------|---------|-------------------|-------------------|------------|------------|------------|------|---------|-------|--------------------|----------|------------|--------------------|-------------------|---------|-----|----------|----|------------------|--------------------|------------|----------|--------------|-------------------|--------------------|
| S US-10-427-715-30 | 5 US-10-721-839-30 | _ | US-10 | 4 US-10-141-645-1 | US-10 | 4 US-10-060-102-32 | 10-141- | US-10-1 | 4 US-10-141-645-4 | US-10-427- | US-10-721- | US-10-141- | us-1 | US-10-0 | US-10 | 5 US-10-427-715-14 | US-10-42 | -10 | 5 US-10-721-839-28 | 4 US-10-141-645-7 | US-10-4 | | US-10-42 | | US-09-917-340-53 | 7 US-10-844-837-53 | | -10-141- | US-10-141-64 | | 5 US-10-427-715-38 |
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| 14 99 88.4 | œ | | 80 | 18 92 82.1 | 80 | 20 89 79.5 | 7 | 7 | 9 7 | 9 7 | 9 7 | 26 88 78.6 | 8 | 9 | 6 7 | 30 86 76.8 | 9/ 9 | 32 86 76.8 | 9 | r. | 4 | - | | • | 71 | 40 80 71.4 | 41 80 71.4 | | 9 | 9 | 45 76 67.9 |
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

ALIGNMENTS

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APPLICANT: STAPLETON, JACK
APPLICANT: STRINKI, MARK
APPLICANT: STRINKI, MARK
APPLICANT: STRINKI, MARK
APPLICANT: STRINKI, MARK
APPLICANT: TRINKI, MARK
APPLICANT: TACK, BRIAN
TITLE OF INVENTION: CATHELICIDINS
FILE REPERENCE: 100A:03508
CURRENT APPLICATION NUMBER: 60/209,368
PRIOR APPLICATION NUMBER: 60/265,270
SOFTWARE: PACENTIN VET. 2.1
SEQ. ID NO 2:
SOFTWARE: PACENTIN VET. 2.1
SEQ. ID NO 2:
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic; CTHER INFORMATION: Peptide US-10-060-102-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 112; DB 14; Best Local Similarity 100.0%; Pred. No. 3.5e-06; Matches 18; Conservative 0; Mismatches 0;
; Sequence 29, Application US/10060102; Publication No. US20030022829A1; GENERAL INFORMATION:
                                                                                               APPLICANT: MAURY, WENDY
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RESULT 5

US-10-721-839-29

US-10-721-839-29

Sequence 29, Application US/10721839

Sequence 29, Application Wo. US20040086535A1

SEQUENCE 20, Application No. US20040086535A1

SEQUENCE 20, WENDY

APPLICANT: STAPLETON, JACK

APPLICANT: STAPLETON, JACK

APPLICANT: TACK, BRIAN

TITLE OF INVENTION: CATHELICIDINS

FILE REPRENSENCE: LOWER 105/10/721,839

CURRENT APPLICATION NUMBER: US/10/706,102

FRIOR APPLICATION NUMBER: 60/309,368

FRIOR PLING DATE: 2001-01-22

PRIOR PLING DATE: 2001-01-30

NUMBER: OF SEQ ID NOS: 32

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 29

LENGTH: 18

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US-10-721-839-29
                                                                    TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs TITLE OF INVENTION: Thereof, and Methods of Use FILE REPERSENCE: 66778-302 (USC554) CURENT APPLICATION NUMBER: US/10/427,715 CURRENT FILING DATE: 2003-04-30 PRIOR PILING DATE: 2002-04-30 NUMBER OF SEQ ID NOS: 41 SOFTHARE: PastSEQ for Windows Version 4.0 SEQ ID NO S: 41 SEQ I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 112; DB 15;
100.0%; Pred. No. 3.5e-06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 112; DB 15; Best Local Similarity 100.0%; Pred. No. 3.5e-06; Matches 18; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: at the C terminus US-10-427-715-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GVCRCLCRRGVCRCLCRR 18
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
APPLICANT: Selsted, Michael E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Conservative
                                                 Tran, Dat Q.
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Best Local Similarity
Matches 18; Conserva
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                                                                                                                                                                                                                                                         Sequence 3, Application US/10427715
Fublication No. US20040014669A1
Fublication No. US20040014669A1
GENERAL INFORMATION:
APPLICANT: Tran, Dat O.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
TILE REFERENCE: 66778-302 (US5754)
CURRENT APPLICATION NUMBER: US 60/377,071
PRIOR FILING DATE: 2003-04-30
PRIOR APPLICATION NUMBER: US 60/377,071
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID MOSS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Score 112; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.5e-06;
Matches 18; Conservative 0; Mismatches 0; Indels
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; OTHER INFORMATION: synthetic construct
US-10-427-715-15
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; Sequence 16, Application US/10427715
; Publication No. US20040014669A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Macaca mulatta
US-10-427-715-3
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LENGTH: 18
TYPE: PRT
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APPLICANT: STAPLENDY
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: ROLLER, MARK
APPLICANT: ROLLER, MARK
APPLICANT: MCRAY, PAUL B.
APPLICANT: MCRAY, PAUL B.
TITLE OF INVENTION: CATHELICIDINS
FILE REFRENCE: IOWA-035U8
CURRENT APPLICATION NUMBER: US/10/721,839
CURRENT FILING DATE: 2003-11-25
FRIOR FILING DATE: 2001-08-01
FRIOR FILING DATE: 2001-08-01
FRIOR FILING DATE: 2001-08-01
FRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN UNBER: 201-01-30
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 31
SEQ ID NO 31
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APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STAPLETON, JACK
APPLICANT: STINSKI, MARK
APPLICANT: STINSKI, MARK
APPLICANT: MCCRAY, PAUL B.
TITLE OF INVENTION: CATHELICIDINS
TITLE OF INVENTION: CATHELICIDINS
TITLE OF INVENTION: 2002-02-22
CURRENT APPLICATION NUMBER: US/10/060,102
CURRENT FILING DATE: 2002-03-22
PRIOR PRILING DATE: 2001-08-01
PRIOR PRILING DATE: 2001-03-03
PRIOR PILING DATE: 2001-03-03
PRIOR PLING DATE: 2001-03-03
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VEY: 2.1
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US-10-721-839-31
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83.3%; Pred. No. 4.5e-05;
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US-10-060-102-30
Sequence 30, Application US/10060102
Publication No. US20030022829A1
GENERAL INFORMATION
                                                                                                                                                                 ; Sequence 31, Application US/10721839; Publication No. US20040086535A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 15; Conservative
                                                                                                                                                US-10-721-839-31
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LENGTH: 18
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TITLE OF INVENTION CATHELICIDINS
TITLE OF INVENTION CATHELICIDINS
TITLE REPERENCE: IOWA:0350S
CURRENT APPLICATION NUMBER: US/10/060,102
CURRENT FILING DATE: 2002-02-22
CURRENT FILING DATE: 2001-08-01
PRIOR PRIOR APPLICATION NUMBER: 60/265,270
PRIOR PILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver: 2.1
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US-10-060-102-31
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                                                     Sequence 17, Application US/10427715
Publication No. US20040014669A1
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Selsted, Michael E.
APPLICANT: Tran, Dat O.
TITLE OF INVENTION: Thereof, and Methods of Use
FILE REFERENCE: 66778-302 (UC5754)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT FILING DATE: 2003-04-30
PRIOR PELING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FREESE for Mindows Version 4.0
LENGTH: 18
TYPE: PRT
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95.5%; Score 107; DB 15;
Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0;
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LOCATION: 18
COTATION: 18
US-10-427-715-17
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Publication No. US20030022829A1
GENERAL INFORMATION:
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LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: STAPLETON, JACK
APPLICANT: STLNER, RICHARD
APPLICANT: STINSKI, MARK
APPLICANT: MCRAY, PAUL B.
APPLICANT: TACK, BRIAN
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Best Local Similarity
Matches 15; Conserv
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Sequence 1, Application US/20162718A1
Sequence 1. Royal Carlon No US20030162718A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fang, Yi-Quan
APPLICANT: Vuan, Jun
APPLICANT: Vuan, Jun
APPLICANT: Obellette, Andre J.
TITLE OF INVENTION: Antimicrobial Theta Defensins and Methods of Using Same FILE REPERENCE: P-UC 3095
CURRENT APPLICATION NUMBER: US/10/313,994
CURRENT FILING DATE: 2002-12-05
PRIOR FILING DATE: 1999-05-10
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    ; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-060-102-30
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Sequence 1, Application US/10427715

Bolication No. US20040014669A1

GENERAL INFORMATION:

APPLICANT: Selsted, Michael E.

TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs

TITLE OF INVENTION: Thereof, and Methods of Use

FILE REFERENCE: 66778-302 (UC5754)

CURRENT APPLICATION NUMBER: US/10/427,715

CURRENT FILING DATE: 2003-04-30

PRIOR PRILING DATE: 2002-04-30

NUMBER OF SEQ ID NOS: 41

SOFTWARE: FASTERQ for Windows Version 4.0

LENGTH: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 99, DB 14; Length 18;
Pred. No. 9.7e-05;
1; Mismatches 2; Indels
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                                                                                                    Score 99; DB 14; Length 18;
Pred. No. 9.7e-05;
1; Mismatches 2; Indels
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                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GVCRCLCRRGVCRCLCRR 18
                                                                                                                                                                                                             1 GVCRCLCRRGVCRCLCRR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
                                                                                                    Query Match
Best Local Similarity 83.3%;
Matches 15; Conservative
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SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Macaca mulatta
US-10-427-715-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Macaca mulatta
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Best Local Similarity
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; Sequence 13, Application US/10427715
; Publication No. USZ0040014669A1
; Publication No. USZ0040014669A1
; GENERAL INFORMATION:
    APPLICANT: Selsted, Michael E.
    APPLICANT: Antimicrobial Theta Defensins, Analogs
    TITLE OF INVENTION: Antimicrobial Theta Defension 4.0
    SEQ ID NO 13
    MENGTH: 18
RESULT 12
'Sequence 12, Application US/10427715
'Sequence 12, Application US/10427715
'Publication No. US20040014669A1
'GENERAL INFORMATION:
'A PAPLICANT: Selsted, Michael E.
'A PAPLICANT: Tran, Dat Q.
'TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
'TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
'TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
'TITLE OF INVENTION: Autimicrobial Theta Defension Analogs
'TITLE OF INVENTION: Autimicrobial Theta Defension Analogs
'TITLE OF INVENTION: Autimicrobial Theta Defension Analogs
'SCOTOM THETA TRANSPORTION: Analogs
'TITLE OF INVENTION: Autimicrobial Theta Defension Analogs
'SCOTOM THETA TRANSPORTION: Analogs
'TITLE OF INVENTION: Autimicrobial Theta Defension Analogs
'TITLE OF INVENTION: Analogs
'TITLE OF INVENTIO
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88.4%; Score 99; DB 15; Length 18;
Best Local Similarity 83.3%; Pred. No. 9.7e-05;
Matches 15; Conservative 1; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Bynthetic construct US-10-427-715-12
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CTHER INFORMATION: at the C terminus
US-10-427-715-13
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Search completed: April 28, 2005, 14:26:50 Job time: 91.5 secs
1 GFCRCLCRRGVCRCICTR 18
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Sublication No. US20040086535A1
GENERAL INFORMATION:
APPLICANT: MAURY, WENDY
APPLICANT: STAPEN, JACK
APPLICANT: STINSKI, MARK
APPLICANT: STINSKI, MARK
APPLICANT: TACK, BRIAN
TITLE OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALITIES OF INVENTION: NOVEL ANTIVIRAL ACTIVITIES OF PRIMATE THETA DEFENSINS AND MAMMALITIES OF INVENTION NUMBER: US/10/721,839
CURRENT FILING DATE: 2003-11-25
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OTHER INFORMATION: Description of Artificial Sequence: Synthetic;
OTHER INFORMATION: Peptide
15-10-721-839-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
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                                                                 Sequence 30, Application US/10427715
Publication No. US20040014669A1
GENERAL INFORMATION;
APPLICANT: Selated, Michael E.
APPLICANT: Tran, Dat Q.
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Antimicrobial Theta Defensins, Analogs
TITLE OF INVENTION: Thereof, and Methods of Use
TILE REFERENCE: 66778-302 (UGS754)
CURRENT APPLICATION NUMBER: US/10/427,715
CURRENT FILING DATE: 2003-04-30
PRIOR PRIOR DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

88.4%; Score 99; DB 15; Length 18;
Best Local Similarity 87.5%; Pred. No. 9.7e-05;
Matches 14; Conservative 2; Mismatches 0; Indels
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88.4%; Score 99; DB 15; Length 18;
Best Local Similarity 83.3%; Pred, No. 9.7e-05;
Matches 15; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
; OTHER INFORMATION: synthetic construct US-10-427-715-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: US/10/060,102
PRIOR FILING DATE: 2002-02-22
PRIOR PILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/265,270
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 18
                                              -10-427-715-30
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 30
LENGTH: 18
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April 28, 2005, 14:00:51 ; Search time 26 Seconds (without alignments) 66.612 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                     OM protein - protein search, using sw model
                                                                                                                                                                                                                                                              US-10-009-317A-33
                                                                                                                                                      Run on:
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283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 112 1 GVCRCLCRRGVCRCLCRR 18 Perfect score: Scoring table: Sequence: Searched:

283416 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

PIR_79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | Description | theta defensin-1 | theta defensin 1b | hypothetical prote | hypothetical prote | О | hypothetical prote | | | hypothetical prote | hypothetical prote | memb | probable integral | G protein-coupled | AcOrf-70 protein - | hypothetical prote | epidermal growth f | transcription fact | Balbiani ring 3 pr | genome polyprotein | otogelin - mouse | Q300 protein - mou | C-8 sterol isomera | nel protein - chic | neurotoxin Tx2 - 8 | pulmonary surfacta | fibronectin recept | hypothetical profe | chloramphenicol re | probable diogenase |
|-----------|------------------|------------------|-------------------|--------------------|--------------------|--------|--------------------|-------|------|--------------------|--------------------|--------|-------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| SUMMARIES | ΩI | : | • | | | 869207 | T15617 | | | | | S50807 | E71602 | JC5042 | G72858 | B70554 | EGMSMG | A41116 | S08167 | GNNY21 | T42214 | 148725 | T46871 | JP0076 | S29214 | LNPG1 | C37057 | D72481 | A25854 | H90942 |
| | Length DB | ' | | | | | | 152 2 | | .85 2 | | 131 2 | | 476 2 | 290 2 | 303 2 | 1217 1 | 265 2 | 1700 2 | 2206 1 | | | | 835 2 | • | | | 28 | 302 2 | 21 |
| de | Query Match I | 71.4 | 53.6 | 51.8 | 50.9 | 47.8 | 46.9 | 46.4 | 45.5 | 45.5 | 45.1 | 44.6 | 44.2 | 43.8 | 42.9 | 42.9 | 42.9 | 42.4 | 42.0 | 42.0 | • | 41.5 | • | 41.5 | 41.1 | 41.1 | 41.1 | 41.1 | 41.1 | 41.1 |
| | Score | 80 | 09 | 58 | 57 | 53,5 | 52.5 | 52 | 51 | 51 | 50.5 | 20 | 49.5 | 49 | 48 | 48 | ₩. | 47.5 | 47 | 47 | 4 | 46.5 | Ġ | 46.5 | 46 | 46 | 46 | 46 | 46 | 46 |
| | Result No. | H | 7 | e | 4 | വ | 9 | 7 | α | 6 | 10 | 11 | 12 | 13 | 14 | 15 | 16 | 17 | . 18 | 19 | | 21 | 22 | 23 | 24 | 25 | 26 | 27 | 28 | 29 |

Library 29-05-1999 #sequence_revision 29-0ct_1999 #text_change 09-Jul-2004
C;Species: Macaca mulatta (rhesus macaque)
C;Species: John 1999 #sequence_revision 29-0ct_1999 #text_change 09-Jul-2004
C;Accession: B59089
R;Tang, Y.Q.; Yuan, J.; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J.
Science 286, 498-502, 1999
A;Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation A;Reference number: A59089; MUID:99453140; PMID:10521339
A;Accession: B59089
A;Accession: B59089
A;Accession: B59089
A;Redues: I-76 <IAN>
A;Redidues: I-76 <IAN>
A;Cross-references: UNIPROT:P82271; GB:AF191101; NID:G6137229; PIDN:AAF04390.1; PID:g61
C;Comment: For the complete mature sequence, see PIR:C59089.
C;Superfamily: mammalian defensin
C;Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing
F;1-20/Domain: signal sequence #status predicted <SIG>

| probable dioxygena probable diogenase | cobyric acid synth epidermal growth f | restrictin precurs proteinase inhibit | Bowman-Birk protei proteinase inhibit | hypothetical prote hypothetical prote | probable dioxygena probable cobQ prot | protein F12K21.20 | ilbrohectin recept hypothetical prote | hypothetical prote |
|---------------------------------------|---------------------------------------|---------------------------------------|---------------------------------------|---------------------------------------|---------------------------------------|-------------------|--|--------------------|
| C64941 D85791 | C82426 EGRT | JH0675 S07405 | JC2225 TISYC2 | T28784 S02186 | AE0304 C70940 | H86468 | D2/0/9 T15840 | 826689 |
| 0 0 | 7 7 | ٦ 7 | 7 7 | ~ ~ | 0 0 | ~ ~ | 9 N | 7 |
| 321 | 484 | 1353 83 | 94 103 | 532 95 | 321 | 602 | 2946 | 118 |
| 41.1 41.1 | 41.1 | 41.1 | 40.6 | 40.6 | 40.2 | 40.2 | 4 4 5 0 7 0 | 39.7 |
| 4 4 6 | 46 46 | 45.5 | 45.5 45.5 | 45.5 45 | 4 4 2 2 | 24.5 | 4.5 | 44.5 |
| | a | -1 10 | 9 6 | m m | | ~ ~ | ۸ 🚙 | |

ALIGNMENTS

| RESULT 1 C59089 theta defensin-1 - N,Alternate names: C;Species: Macaca m C;Date: 29-Oct-1999 C;Accession: C59089 R;Tang, YO, Yuan, Science 286, 498-50 A;Title: A cyclic a A;Reference number: A;Accession: C59089 | RESULT 1 C59089 Letera defensin-1 - rhesus macaque N;Alternate names: RTD-1 C;Species: Macaca mulatta (rhesus macaque) C;Species: Macaca mulatta (rhesus macaque) C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Date: 29-Oct-1999 R;Tang, Y.O.; Yuan, J; Osapay, G.; Osapay, K.; Tran, D.; Miller, C.J.; Ouellette, A.J. Science 286, 498-502, 1999 A;Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation A;Reference number: A59089; MUID:99453140; PMID:10521339 A;Status: preliminary |
|---|--|
| A. Residues A. Note: th: C. Comment C. Keywords: F:1-9/Regid F:1-18/Reg F:1-18/Reg F:2-11,4-9 | A;Residues: 1.18 45ED. A;Note: this sequence is cyclically permuted by -6 residues from the sequence presented C;Comment: the two contributing precursor sequences, see PIR:A59089 and PIR:B59089. C;Comment: For the two contributing precursor sequences, see PIR:A59089 and PIR:B59089. C;Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing F;1-9/Region: theta defensin la-derived F;10-18/Region: theta defensin lb-derived F;1-18/Cross-link: cyclopeptide (Arg-Cys) #status experimental F;2-11,4-9,13-18/Disulfide bonds: #status experimental F;2-11,4-9,13-18/Disulfide bonds: #status experimental |
| Query Match Best Local Matches 1 Qy 4 | Ouery Match 71.4%; Score 80; DB 2; Length 18; Best Local Similarity 80.0%; Pred. No. 0.0015; Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0; 4 RCLCRRGVCRCLCRR 18 |

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vascular endothelial growth factor C precursor - human
NyAlternate names: FLT4 ligand DHM
C;Species: Homo sapiens (man)
C;Date: 27-Apr-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C;Accession: 869207; 861795; $71444; 869208; G02659
R;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela, E;Joukov, V.; Pajusola, K.; Kaipainen, A.; Chilov, D.; Lahtinen, I.; Kukk, E.; Saksela, A;Title: Corrigendum: A novel vascular endothelial growth factor, VEGF-C, is a ligand f A;Reference number: 869207
A;Reference number: 869207
A;Accession: 869207
A;Accession: 869207
A;Accession: 869207
A;Accession: 869207
A;Accession: 869207
A;Residues: 1-419 <JOUV
A;Residues: 1-419 <JOUV
A;Residues: 1-419 <JOUV
A;Cross-references: Untracorride sequence of the EMBL Data Library, December 1995
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
A;Note: this is a revision to the sequence from reference 861795
A;Note: this is a revision to the sequence from reference 861795
B;Note: this is a revision to the sequence from reference 861795
A;Note: this is a revision to the sequence from reference 861795
A;Note: this is a revision to the sequence from reference 861795
A;Note: this is a revision to the sequence from reference 861795
A;Reference number: 861795; MUID:96170224; PMID:8617204
A;Reference number: 861795; MUID:96170224; PMID:8617204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 'X',104-120 <J0002>
R;Lee, J.; Gray, A.; Yuan, J.; Luoh, S.M.; Avraham, H.; Wood, W.I.
submitted to the EMBL Data Library, December 1995
A;Description: Vascular endothelial growth factor related protein (VRP): A ligand and A;Reference number: S69208
A;Accession: S69208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: S61795
A;Accession: S61795
A;Accession: S61795
A;Nolecule type: mRNA
A;Residues: 70-419 <0001>
A;Note: this sequence has been revised in reference S69207
A;Accession: S71443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F:1-12/Domain: signal sequence #status predicted <SIG>
F:13-102/Domain: propeptide #status predicted <PRO>
F:103-419/Product: vascular endothelial growth factor C #status experimental <MAT>
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A, Residues: 1-419 < LEE>
A, Residues: 1-419 < LEE>
A, Cross-references: EMBL: U43142; NID: g1150988; PIDN: AAA85214.1; PID: g1150989
A, Cross-references: EMBL: Data Library, May 1996
A, Reference number: H01557
A, Reference number: H01557
A, Returns: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-419 < MONS.
A, Cross-reference number: H119 < MONS.
A, Cross-reference number: H119 < MONS.
A, Molecule type: mRNA
A, Residues: 1-419 < MONS.
A, Cross-reference number: H119 < MONS.
A, Molecule type: mRNA
A, Residues: H119 < MONS.
A, Molecule type: MONS.
A, M
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C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C25F6.2 - Caenorhabditis elegans Cispecies: Caenorhabditis elegans Cispecies: Caenorhabditis elegans Cjaceise: Caenorhabditis elegans Cjacesion: T1567 Especies: Caenorhabditis elegans Cjacession: T1567 Especies: Caenorhabditis elegans Corper 1995 Aspecies to the EMBL Data Library, October 1995 Aspecription: The sequence of C. elegans cosmid C25F6. Aspeciation: T15617 Aspecsion: T15617 Aspecsion: T15617
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291 CQCVCRAGLRPASCGPHKELDRNSCQCVCK 320
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26.7%; Pred. No. 14;
:ive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CRCLCRRGV------CRCLCR 17
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A;Cross-references: GDB:3890883; OMIM:601528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 26.7 nes 8; Conservative
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-164 <WIL>

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A,Statuus: preliminary; translated from GB/EMBL/DDBJ
A,Ratiques: DNA
A,Residues: 1-188 <NHA>
A,Cross_references: UNIPROT:Q18238; EMBL:U58760; NID:g1330384; PID:g1330389; PIDN:AAB007
A,Expinimental gource: strain Bristol N2; clone C27A2
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein C27A2.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15651
R;Nhan, M.
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T24272
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                                            F;21-64/Domain: amino-terminal propeptide #status predicted <PRO>F;74-76/Domain: carboxyl-terminal propeptide #status predicted <CTP>
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                                                                                                                                                                                  DB 2; Length 76;
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A; Description: The sequence of C. elegans cosmid C27A2.
A; Reference number: 218382
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A,Reference number: Z19867
                                                                                                                                                                                  / Match 53.6%; Score 60; DB Local Similarity 83.3%; Pred. No. 0.81 Les 10; Conservative 1; Mismatches
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Pred. No.
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Pred. No.
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Best Local Similarity
Matches 10; Conserv
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A; Introns: 20/3; 90/2
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A,Map position: 2
A,Introns: 19/3; 91/2
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Best Local S
Matches 10
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Matches
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Appointerical protein 2 - mouse
C,Species: Mus musculus (house mouse)
C,Decies: 30-8ep-1993 #sequence_revision 30-8ep-1993 #text_change 09-Jul-2004
C,Accession: B45878
R,Sarvetnick, N.; Tsai, J.Y.; Fox, H.; Pilder, S.H.; Silver, L.M.
Immunogenetics 30, 34-41, 1989
A,Title: A mouse chromosome 17 gene encodes a testes-specific transcript with unusual p
A,Reference number: A45878; MUID:89307395; PMID:2568335
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NAlternate names: hypothetical protein HRC131; hypothetical protein J1120

Species: Saccharomyces cerevisiae

C;Date: 13-Jan-1995 #sequence revision 08-Sep-1995 #text_change 09-Jul-2004

C;Accession: SS6007; S47126; S5638

R;Vandenbol, M; Durand, P; Dion, C; Portetelle, D; Hilger, F.
Yeast 11, 57-60, 1995

A;Title: Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisi

A;Title: Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisi

A;Reference number: S50798; MUID:95282514; PMID:7762302

A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                      hypothetical protein F16M2.210 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date 20. Apr 2000 #sequence_revision 20-Apr 2000 #text_change 09-Jul-2004 C;Accession: T48125 R;Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, submitted to the Protein Sequence Database, April 2000 A;Reference number: Z24459 A;Accession: T48125
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A;Molecule type: mRNA
A;Residues: 1-582 <SAR.
A;Cross-references: UNIPROT:Q62295; GB:M28821
A;Note: this sequence has been corrected in Immunogenetics 31, 283-284 (1990)
C;Superfamily: mouse hypothetical protein 2
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                                                                                                                                                                                                                                                                                                                                                                                               Score 51; DB 2;
Pred. No. 9.6;
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44.4%; Pred. No. >...
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 GLCDNLCKYEGAISGVCVSDPHRCLCR 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12; Conservative
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Matches 9; Conservative
        65 RCICTRGFCRLL 76
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Best Local Similarity
Matches 12; Conserv
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A; Note: F16M2.210
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A;Accession: T18975
A;Status: prelimary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-152 <WIL>
A;Cross-references: UNIPROT:Q9XVX3; EMBL:Z49886; PIDN:CAA90055.1; GSPDB:GN00020; CESP:CGA;Experimental source: clone C06Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-76 cTAN-
A;Cross-references: UNIPROT:P82270; GB:AF191100; NID:g6137227; PIDN:AAF04389.1; PID:g613
C;Comment: For the complete mature sequence, see PIR:C59089.
A,Molecule type: DNA
A,Residues: 1-1131 <BEN>
A,Cross-references: EMBL:U39742; NID:g1049455; PID:g1049459; PIDN:AAA80434.1; CESP:C25F6
                                                                             C;Genetics:
A;Gene: CESP:C25F6.2
A;Introns: 105/1; 210/3; 283/3; 316/1; 346/2; 463/3; 566/1; 722/2; 897/1; 991/2; 1032/1;
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A;Title: A cyclic antimicrobial peptide produced in primate leukocytes by the ligation of A;Reference number: A59089; MUID:99453140; PMID:10521339
A;Scatus: preliminary
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C; Keywords: antibacterial; antibiotic; antifungal; leukocyte; protein splicing
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-64/Domain: amino-terminal propeptide #status predicted <PRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein C06Al.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  theta defensin la precursor - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 29-Oct_1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
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Pred. No. 8.9;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                      Indels
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Pred. No. 11;
0; Mismatches 8
                                                                                                                                                                                             46.9%; Score 52.5; Dilarity 47.1%; Pred. No. 33; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, June 1995
A;Reference number: Z19054
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Best Local Similarity
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 9; Conserv
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A;Map position: 2
A;Introns: 22/3
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C;Genetics:

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Gaps

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Indels

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Score 49; DB 2; Length 476; Pred. No. 49;
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442 LCKCVCRRGAMERRFRR 458
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nes 8; Conservative
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A;Molecule type: DNA
A;Residues: 1-290 <AYR>
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               A;Cross-references: UNIPROT:P47038; EMBL:234288; NID:g498992; PIDN:CAA84058.1; PID:g4990 A;Note: the nuclectide sequence was submitted to the EMBL Data Library, June 1994 Skyandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F. submitted to the EMBL Data Library, June 1994 A;Description: Sequence analysis of a 17.1 kb DNA fragment from chromosome X of Sacchard A;Reference number: 847117
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A;Cross-references: UNIPROT:O96282; GB:AE001428; GB:AE001362; NID:93845316; PIDN:AAC719<sup>-</sup>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable integral membrane protein PFB0950w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falcibarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Species: Plasmodium falciparum
C; Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C; Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C; Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C; Accession: E71602
R; Gardner, M.J.; Tettellin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.; Pertea, M.J.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, 18-clance 283, 1126-1132, 1998
A; Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum. A; Reference number: A71600; MUID:99021743; PMID:9804551
A; Accession: E71602
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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A;Accession: S56838
A;Molecule type: DNA
A;Residues: 1-131 <POH>
A;Cross-references: EMBL:Z49340; NID:g1008212; PID:g1008214; MIPS:YJL064w
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C;Superfamily: Saccharomyces probable membrane protein YJL064w
C;Keywords: transmembrane protein
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A;Molecule type: DNA
A;Residues: 1-131 «VAM»
A;Cross-references: EMBL:Z34288; NID:g49892; PID:g499002
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F. submitted to the Protein Sequence Database, September 1995
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7
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Best Local Similarity 52.9%; Pred. No. 17;
Matches 9; Conservative 0; Mismatches
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Acorf-70 protein - Autographa californica nuclear polyhedrosis virus CiSpecies: Autographa californica nuclear polyhedrosis virus, AcMNPV A,Note: dsDNA virus C,Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004 C,Accession: G72658 R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D. Virology 202, 586-605, 1994 A,Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus A,Reference number: A72850; MuID:94303173; PMID:8030224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein Rv1145 - Mycobacterium tuberculosis (strain H37RV)
C; Species: Mycobacterium tuberculosis
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C; Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C; Dacession: B70554
R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Whitehead, S.; Barrell, B.G.
A; Atlie: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A; Reference number: A70500; MUID:98295987; PMID:9634230
A; Accession: B70554
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-33 <COL>A; Residues: 1-33 <COL>A; Residues: 1-33 <COL>A; Residues: 1-33 <COL>A; Reperimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Cross-references: UNIPROT:P41470; GB:L22858; NID:9510708; PIDN:AAA66700.1; PID:955913
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C;Genetics:
A;Gene: Rv1145
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0; Gaps Query Match Best Local Similarity 60.0%; Pred. No. 48; Matches 9; Conservative 0; Mismatches 6; Indels

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Search completed: April 28, 2005, 14:22:38 Job time: 27 secs

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brachydanio caenorhabdi

drosophila

homo sapien xenopus lae macaca mula arabidopsis macaca fasc sinorhizobi

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mus musculu burkholderi

263mq5

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Result

Perfect score:

Run on:

Sequence:

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TISSUB-TORQUE;
Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
Wakebe H., Ono T., Habigaki H., Watanabe T., Ozaki K., Sugiyama T.,
Irie R., Otsuki T., Sato H., Wakamateu A., Ishii S., Yamamoto J.,
Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
Yamachita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
Wagatsuma M., Murakawa K., Kanchori K., Takahashi-Fujii A., Oshima A.,
Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K.,
Masubo Y., Nagai K., Isogai T.;
Submitted (Mak-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AKIJ1548; BAD18682.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCB_TaxID=9606;
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P82271;
25-OCT-2004 (Rel. 45, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
25-OCT-2014 (Rel. 45, Last annotation update)
Theta defensin-1, subunit B precursor (RTD-1b) (Demidefensin 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypothetical protein FLJ16784.
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O; GO:007242; P:intracellular signaling
InterPro; IPR008973; C2 CalB.
InterPro; IPR002219; DAG_PE-bind.
                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
06GQP2
09XVX3
09XVX3
081C10
081C18
07PC24
08PW14
0819G7
091BG7
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  SMART; SM00109;
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                           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1 GVCRCLCRRGVCRCLCRR 18
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1: uniprot_sprot:*
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Length 243;

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Adachi J., Aizawa K., Akimura T., Arai A., Aono H.,

Adachi J., Aizawa K., Akamura T., Fukunishi Y., Furuno M.,

Arakawa T., Bono H., Carninoi P., Fukuda S., Fukunishi Y., Furuno M.,

Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

Asaaki D., Shibata K., Shibata W., Sakai C., Sakai K.,

Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

A Muramatsu W., Hayashizaki Y.,

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

MGD, MGI:1113992; 4931420D14Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
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SETRANT=CS7BL/G1 TISSUE=Testis;
MEDLINE=CS7BL/G1 TISSUE=Testis;
MEDLINE=C914; 99374; PubMed-1042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Monto H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Monto H., Okazaki Chibaratsu M., Hayashizaki Y.;
Monto H., Dibaratsu M., Hayashizaki Y.;
Monto H., Chibaratsu M., Hayashizaki M., Hayashizaki Y.;
Monto H., Chibaratsu M., Hayashizaki Y.;
Monto H., Chibaratsu M., Hayashizaki M., H
                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CS7BL/6G; TISSUE=Testis;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=C57BL/64; TISSUE=Testis; MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sunbata W., Itoh W., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mateumoto H., Sakaguchi S., Ikogami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Mateuura S., Kawai J., Rikik lintegrated sequence and Y., Kira A., Hayashizaki Y.; Rikik lintegrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:1700055105 product:hypothetical Cysteine-rich region
Containing protein, full insert sequence.
Name-4931420D14Rik;
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM CONSORTIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 420:563-573 (2002).
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                                                                                                                                                                                                   Mus musculus (Mouse)
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      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                    DEVELOPMENTAL STAGE, AND DISULFIDE BONDS.

DEVELOPMENTAL STAGE, AND DISULFIDE BONDS.

TISSUE=Bone marrow, and Leukocyte;

MEDLINE=B04453140; PubMed=10521339; DOI=10.1126/science.286.5439.498;

Tang Y.-Q., Yuan J., Osapay G., Osapay K., Tran D., Miller C.J.,

Quellette A.J., Selsted M.E.;

"A cyclic antimicrobial peptide produced in primate leukocytes by the ligation of two truncated alpha-defensins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

TISSUB-Bone marrow;

TISSUB-Bone marrow;

Zhao C., Nguyen T., Lehrer R.I.;

"cDNA cloning of three alpha-defensins and three demidefensins from rheaus monkey bone marrow.";

Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

-I-FUNCTION: Active against Gram-positive bacteria S.aureus and I. monocytogenes, Gram-negative bacteria S.typhimurium and B.coli Mils and fungi C.albicans and C.neoformans in vitro.

-I-SUBUNIT: Forms a cyclic heterodimer composed of subunits A and B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pram; PF00879; Defensin propep; 1.
PROSITE; PS00269; DEFENSIN; FALSE NEG.
Antibiotic; Defensin; Direct protein sequencing; Fungicide; Signal.
22 Potential.
                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      À.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: This is a cyclic peptide.
SIMILARITY: Belongs to the corticostatin/defensin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Theta defensin-1, subunit B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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Pred. No. 1.3;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
Q9D912
1D Q9D912
AC Q9D912; PRELIMINARY; PRT;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF191101; AAF04390.1; --
EMBL; AF191103; AAF04382.1; --
EMBL; AF194156; AAF07923.1; --
PIR; B59089; B59089.
                                   Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8189 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                  Cercopithecinae; Macaca.
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65
74
66
68
76 AA;
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Query Match SEQUENCE

Best Loca Matches

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Hypothetical protein.

Gaps

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7; Indels

173 AA.

PRT;

Xu P.-X.;

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STRAIN=C57BL/6J; TISSUE=Testis; MEDLINE=20499374; Pubmed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; Pubmed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(200).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CS7BL/6J; TISSUB=Testis;
MEDIINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninol.P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TrEMBLTE1. 17, Last sequence update)
01-OCT-2002 (TrEMBLTE1. 22, Last annotation update)
Mus musculus adult male testis cDNA, RIKEN full-length enriched
library, clone:4331420014 product:hypothetical Cysteine-rich region
Containing protein, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CS7BL/6J; TISSUE=Testis;
The PANTOW Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
Hanalysis of the mouse transcriptome based on functional annotation
60,770 full-length cDNAs.";
                        Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CS7BL/6J; TISSUB=Testis;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
MEXEN PRAIOM CONSORTIUM;
"Functional amnotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                             51.8%; Score 58; DB 2; Length 168; 56.2%; Pred. No. 4.6;
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STRAIN=C57BL/6J; TISSUE=Testis;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
                                                                                                                                                  STRAIN-CD-1; TISSUE-Testis; Xu X., Bai X., Slvius D., Escalier D., McFarland L., Xu Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF465502; AAO15675.1; -. MGD; MGI:1913992; 4931420D14Rik. SEQUENCE 168 AA; 18957 MW; 8F30D3D27B9BF595 CRC64;
                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
      Name=4931420D14Rik; Synonyms=Cktlr3;
                                                                                                                                                                                                                                                                                                                                                                                                  3 CRCLCRRGVCRCLCRR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                          CRCCCYCRCCRCCSR 81
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                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
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ses 9; Conserv
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                                                                                            NCBI_TaxID=10090;
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Q9D4K2;
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Matches
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Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Altasher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haish F.N.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKernan K.J., Make J.A., Gunzante P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Allalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Mithing M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Mithing M. Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,
Jones S.J., Marra M.J.,
Johes S.J., Marra M.J.,

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                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                            Length 168;
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                                                                                       7; Indels
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EMBL; BC061079; AAH61079.1; -.
SEQUENCE 168 AA; 18947 MW; B00FD3D27B9BF768 CRC64;
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18931 MW; 7A2BD279612A5E94 CRC64;
                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
Basic protein CKTIR3.
                                            DB 2;
                                          53.6%; Score 60; DB 2 '56.2%; Pred. No. 2.6; ative 0; Mismatches
                                                                                                                                                                                                                                                                                      168 AA.
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0; Mismatches
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                                                                                                                             3 CRCLCRRGVCRCLCRR 18
                                                                                                                                                                        66 CRCCCHCRCCRCCCSR 81
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                 Duery Match
Best Local Similarity '56.2%,
Conservative
Conservative
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Director MGC Project;
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168 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                  Name=4931420D14Rik;
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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SEQUENCE
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Q8CH20;
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Q8CH20
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Wilson R.;
Submitted (JUN-2004)
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   STRAIN-Bristol N2;
                                                                  SEQUENCE FROM N.A. STRAIN=Bristol N2;
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                                                                                                                                                                              SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Adachi J., Aizawa K., Akimura T., Arai A., Aono H.,

Adachi J., Aizawa K., Akahira S., Akimura T., Fukunishi Y., Furuno M.,

A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

A Sagaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

A Sogabe Y., Suzuki H., Tagami M., Shibata Y., Shinagawa A., Takahashi F.,

Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

A Muramatsu M., Hayashizaki Y.,

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL, AKO16667; BAB302331; -.

R MGD; MGI:1913992, 4931420D14Rik.
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., "RIKE integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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Wormhase Consortium;
"Genome sequence of the nematode C. elegans: a platform for
"merinating biology. The C. elegans Sequencing Consortium.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.8%; Score 58; DB 2; Length 173; 56.2%; Pred. No. 4.7; 7; Indels tive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The sequence of C. elegans cosmid C27A2.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
REGUENCE 173 AA; 19581 MW; 147B6F155AC29FDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein C27A2.5.
Name-C27A2.5; ORFNames=C27A2.5;
Caenorhabditis elegans.
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MEDLINE-99069613; PubMed-9851916;
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Science 282:2012-2018(1998).
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Best Local Similarity 56.23
Matches 9; Conservative
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SEQUENCE FROM N.A.
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Gaps
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                      WormPep; C27A2.5; CE04105.

GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005613; P:defense response; IEA.
InterPro; IPR001450; 4Fe4S ferredoxin.
InterPro; IPR001007; WWP C.
PROSITE; PS00198; 4Fe4S FERREDOXIN; UNKNOWN 1.
PROSITE; PS00269; DEFENSIN; 1.
PROSITE; PS01269; WWPC_1; UNKNOWN_1.
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Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; Z66499; CAA91301.1; -.
PIR; T24272; T24272.
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to the EMBL/GenBank/DDBJ databases.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Wormpep; T01B7.8; CB03592.
InterPro; IPR0001450; 4Fe4S_ferredoxin.
InterPro; IPR006081; Defensin_alpha.
InterPro; IPR001007; WPF_C.
INCOSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
PROSITE; PS00269; DEFENSIN; UNKNOWN_1.
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STRAIN-Bristol N2;
MEDLINE-99069613; PubMed-9851916;
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ORFNames=T01B7.8;
                                                                                                                                                           WormBase Consortium;
Submitted (SEP-2004) to th
EMBL; US8760; AAK31463.1;
PIR; T15651; T15651.
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nes 10; Conservative
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10; Conservative
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STRAIN=Bristol N2;
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01-OCT-2001
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                                                                              RESULT 10
Q17641
  Matches
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium.";
                                                        Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 166;
                                                                              8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Bristol N2;
Anderson K., Chissoe S.;
"The sequence of C. elegans cosmid CO4G6.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.8on R.; submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
                      Hypothetical protein. - SEQUENCE 164 AA; 16499 MW; C002D48D36C9FCED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16971 MW; 9D9D130351BB50F1 CRC64;
                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DR 2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein C04G6.10
Name=C04G6.10; ORFNames=C04G6.10;
Caenorhabditis elegans
                                                     Query Match 50.9%; Score 57; DB 2; Best Local Similarity 55.6%; Pred. No. 6; Matches 10; Conservative 0; Mismatches 8
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PROSITE; PS00269; DEFENSIN; UNKNOWN 1.
PROSITE; PS01022; EGF 1; UNKNOWN 1.
HYPOTHEICAL PTOTE: 1, UNKNOWN 1.
HYPOTHEICAL PTOTE: 1.
SEQUENCE 166 AA; 16971 MW; 9D9D130351BBSOF
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                                                                                                                                                                                 166 AA.
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InterPro; IPR006081; Defensin_alpha.
InterPro; IPR005209; EGF like.
InterPro; IPR001007; WWP_C.
 PROSITE; PS00022; EGF 1; UNKNOWN 1.
PROSITE; PS01208; VWFC_1; UNKNOWN_1.
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WormPep; C04G6.10; CE27649.
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STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
                                                                                                   1 GVCRCLCRRGVCRCLCRR 18
                                                                                                                        80 GGCCCCRPRCCCCRR 97
                                                                                                                                                                                                                                                                                                                                                                             investigating biology. The C
Science 282:2012-2018(1998).
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                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                        VormBase Consortium;
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Best Local Similarity
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PROSITE;
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  Indels
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Anderson K., Chissoe S.;
"The sequence of C. elegans cosmid CO4G6.";
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WormBase Consortium;
Submitted (SEP-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; U55854; AAK68161.1; -.
HSSP; P10969; 1WGT.
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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PROSITE; PS00269; DEFENSIN; UNKNOWN 1.
PROSITE; PS01208; VWFC_1; UNKNOWN 1.
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Mismatches
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InterPro; IPR006081; Defensin_alpha.
InterPro; IPR006209; EGF_like.
InterPro; IPR001007; VWF_.
                                                                                                                                                                                                                                                            Created)
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MEDLINE=99069613; PubMed=9851916;
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                                            1 GVCRCLCRRGVCRCLCRR 18
                                                                                           GGCGCCCCRPRCCCCCRR 98
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Matches 10; Conservative
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Q949G1

RESULT 11 0949G1

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MEDLINE=91333007; PubMed=1651403;
Teo I.A., Griffin B.E., Jones M.D.;
"Characterization of the DNA polymerase gene of human herpesvirus 6.";
J. Virol. 65:4670-4680(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Martin M.E.D., Nicholas J., Thomson B.J., Newman C., Honess R.W.; "Identification of a transactivating function mapping to the putative immediate-early locus of human herpesvirus 6.";
                                                                                                                                                                                                                                         Littler B., Lawrence G., Liu M.Y., Barrell B.G., Arrand J.R., "Identification, cloning, and expression of the major capsid protein gene of human herpesvirus 6.";
                                                                                                                                                                                                                                                                                                                                                                                                                                      "Human herpesvirus 6 is closely related to human cytomegalovirus.";
J. Virol. 64:287-299(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-92146942; PubMed=1310766; Geng Y., Chandran B., Josephs S.F., Wood C.; Identification and characterization of a human herpesvirus 6 gene segment that trans activates the human immunodeficiency virus type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-91226542; PubMed=1851252; DOI=10.1038/351078a0; Thomson B.J., Efstathiou S., Honess R.W.; "Acquisition of the human adeno-associated virus type-2 rep gene
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MEDLINE=22260671; PubMed=1374813;
Neipel F., Ellinger K., Fleckenstein B.;
"Gene for the major antigenic structural protein (p100) of human
                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90080132; PubMed=2152817;
Lawrence G.L., Chee M., Craxton M.A., Gompels U.A., Honess R.W.,
                                                                                                             RNA stage; Herpesviridae;
01, Created)
01, Last sequence update)
22, Last annotation update)
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MEDLINE=91374590; PubMed=1654446;
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                                                                                                           Viruses, dsDNA viruses, no RNA st
Betaherpesvirinae, Roseolovirus.
NCBI_TaxID=10368;
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J. Virol. 66:3918-3924(1992)
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Nature 351:78-80(1991).
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                   (TrEMBLrel. (TrEMBLrel.
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                                                                                               Human herpesvirus 6.
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 01-NOV-1996
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                                                                           Name=U88;
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                                                                                                                                                                                                                                                                                      MEDLINE=21329048; PubMed=11435398; DOI=10.1101/gr.GR-1617R; Mayber K., Murphy G., Tarchini R., Wambutt R., Volckaert G., Pohl T. Duesterhoeft A., Stiekema W., Entian K.D., Terryn N., Lemcke K., Haase D., Hall C.R., van Dodeweerd A.M., Tingey S.V., Mewes H.W., Bevan M., Bancroft I.; Changey S.V., Mewes H.W., "Conservation of microstructure bewtween a sequenced region of the genome of rice and multiple segments of the genome of Arabidopsis thaliana.";
                                                                                                                                                                           Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Zhang Y., Liu M., He F.;
Exbaritted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF111848; ARF16687.1; -.
SEQUENCE 190 AA; 21480 MW; 4B8104A29AA33844 CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Gramene; Q949G1; -.
Hypothetical protein.
SEQUENCE 274 AA; 28657 MW; ABS47D9BDS470AE1 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                           01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein C15ERIPDM.
Name=C15ERIPDM;
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01-DEC-2001
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ID Q69566
AC Q69566;
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RESULT 12

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RESULT 13

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                       MEDLINE=94025598; PubMed=8212582;
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Q6RY99
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                                                                                                                                                                                                                                              Thomson B.J., Honess R.W.;
"The right end of the unique region of the genome of human herpesvirus 6 Ullo2 contains a candidate immediate early gene enhancer and a homologue of the human cytomegalovirus US22 gene family.";
J. Gen. Virol. 73:1649-1660(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gompels U.A., Carrigan D.R., Carss A.L., Arno J.; "Two groups of human herpesvirus 6 identified by sequence analyses of laboratory strains and variants from Hodgkin's lymphoma and bone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93323202; PubMed=7687301;
Pfeiffer B., Berneman Z.N., Neipel F., Chang C.K., Tirwatnapong S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pellett P.E., Sanchez-Martinez D., Dominguez G., Black J.B., Anton Greenamoyer C., Dambaugh T.R.;
"A strongly immunoreactive virion protein of human herpesvirus 6 variant B strain 229: identification and characterization of the ge and mapping of a variant-specific monoclonal antibody reactive
                                            Efstathiou S., Lawrence G.L., Brown C.M., Barrell B.G., "Identification of homologs to the human cytomegalovirus US22 gene family in human helpesvirus-6."; J. Gen. Virol. 73:1661-1671(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thompson J., Choudhury S., Kashanchi F., Doniger J., Berneman Z., Frenkel N., Rosenthal L.J.; A transforming fragment within the direct repeat region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification and mapping of the gene encoding the glycoprotein complex gp82-gp105 of human herpesvirus 6 and mapping of the neutralizing epitope recognized by monoclonal antibodies."; J. Virol. 67:4611-4620(1993).
                                                                                                                                             Bllinger K., Neipel F., Foa-Tomasi L., Campadelli-Fiume G.
Pleckenstein B.;
                                                                                                                                                                    "The glycoprotein B homologue of human herpesvirus 6."; J. Gen. Virol. 74:495-500(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               herpesvirus type 6 that transactivates HIV-1."
Oncogene 9:1167-1175(1994).
                                                                                                                                                                                                                                                                                                                                               MEDLINE=93091236; PubMed=1333836;
                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=U1102;
MEDLINE=94181269; PubMed=8134119;
MEDLINE=94181269; PubMed=8134119;
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                                   MEDLINE=92333249; PubMed=1321206;
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MEDLINE=93187613; PubMed=8383182;
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J. Gen. Virol. 74:613-622(1993).
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Virology 195:521-531(1993)
[17]
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Zhou Y., Chang C.K., Qian G., Chandran B., Wood C.; "trans-activation of the HIV promoter by a cDNA and its genomic clones of human herpesvirus-6.";
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Thomson B.J., Dewhurst S., Gray D.;
"Structure and heterogeneity of the a sequences of human herpesvirus 6 strain variants U1102 and Z29 and identification of human telomeric repeat sequences at the genomic termini.";
J. Virol. 68:3007-3014(1994).
                                                                                                                                                                                                                                                                                                        Liu D.X., Gompels U.A., Nicholas J., Lelliott C.;
"Identification and expression of the human herpesvirus 6 glycoprotein
H and interaction with an accessory 40K glycoprotein.";
J. Gen. Virol. 74:1847-1857(1993).
Jones M., Teo I.; "Identification and analysis of the transport/capsid assembly protein (tp/cap) gene of human herpsvirus-6 (HHV-6)."; virology 197:449-454(1993).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gompels U.A., Macaulay H.A.; "Characterisation of human telomeric repeat sequences from human herpesvirus-6 and relationship to replication."; J. Gen. Virol. 76:451-458(1995).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,

Kanehori K., Ishibashi T., Chiba Y., Fujimori K., Hiraoka S.,

Kanehori K., Ishibashi T., Sato H., Matanabe M.,

Sugiyama T., Irie R., Otsuki T., Sato H., Makamatsu A., Ishii S.,

Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,

Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,

Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

Suzuki Y., Sugano S., PaReffill;

InterPro; IPR06209; EGF_1ike.

PROSITE: PS01186; EGF_2; UNKNOWN 1.

SEQUENCE 201 AA; 20938 MW; 3408F8E817AA0500 CRC64;
                                                                       Andriamampandry C., Taleb O., Viry S., Muller C., Humbert J.P.,
Gobaille S., Aunis D., Maitre M.,
"Cloning and characterization of a rat brain receptor that binds the
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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49.6%; Score 55.5; DB 2; Length 512;
Best Local Similarity 64.7%; Pred. No. 25;
Matches 11; Conservative 1; Mismatches 4; Indels
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Best Local Similarity 53.3%; Pred. No. 13;
Matches 8; Conservative 2; Mismatches 5; Indels
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                                                                                                                              endogenous neuromodulator gamma-hydroxybutyrate.";
FASEB J. 0.0-0(2004).
EMBL; AY48593; AAR24072.1; -.
GO; GO:00064812; F:receptor activity; IEA.
InterPro; IPR001209; Ribosomal S14.
InterPro; IPR001009; Ribosomal S14.
InterPro; IPR000301; Transmem_4.
PRINTS; PR00259; TWFOUR.
PROSITE; PS00527; RIBOSOMAL_S14; UNKNOWN_1.
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                                                      STRAIN-Wistar; TISSUE-Hippocampus;
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